Fig. 1

	Chimeric blend A	Chimeric blend B
pH	5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0	5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 M

6kb

Fig. 2

6kb BG
15"/kb - 1'-30"

1X Cloned buffer

pH   9.5   10.0   10.5   10.8   11.0   11.5   11.8   12.0

M

6kb ⟶
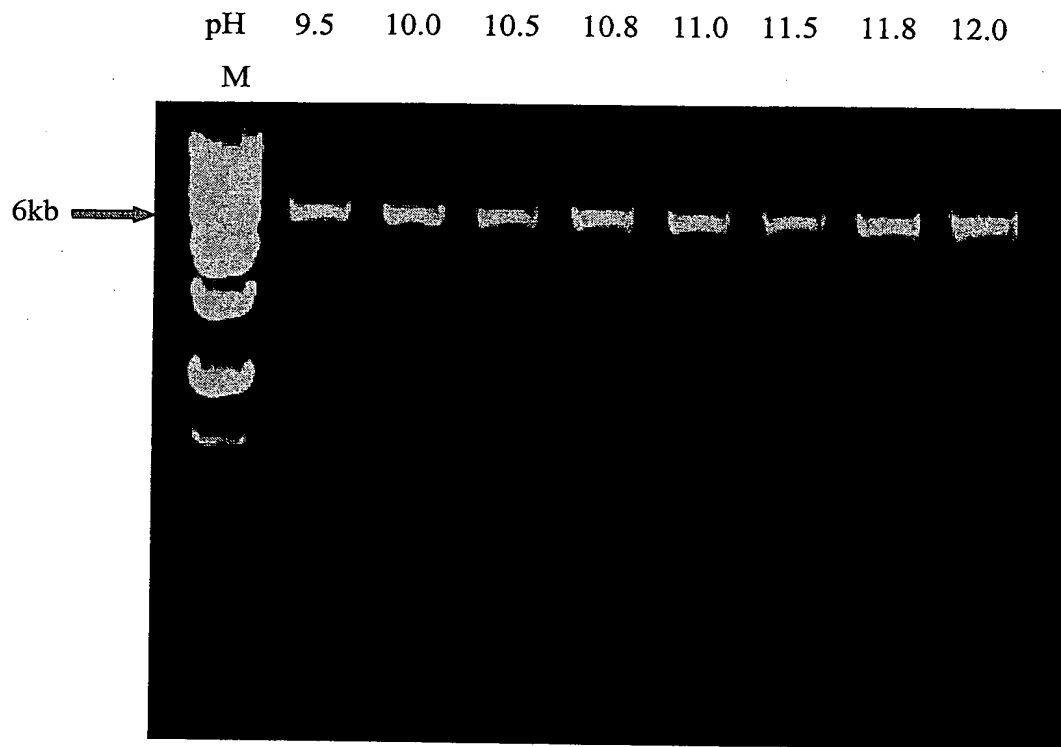
2/186.

Fig. 3

19kb BG
30"/kb - 9.5' extension

	M	pH 10.0		pH 11.8		1.5X Cl	
		1	2	3	4	5	6
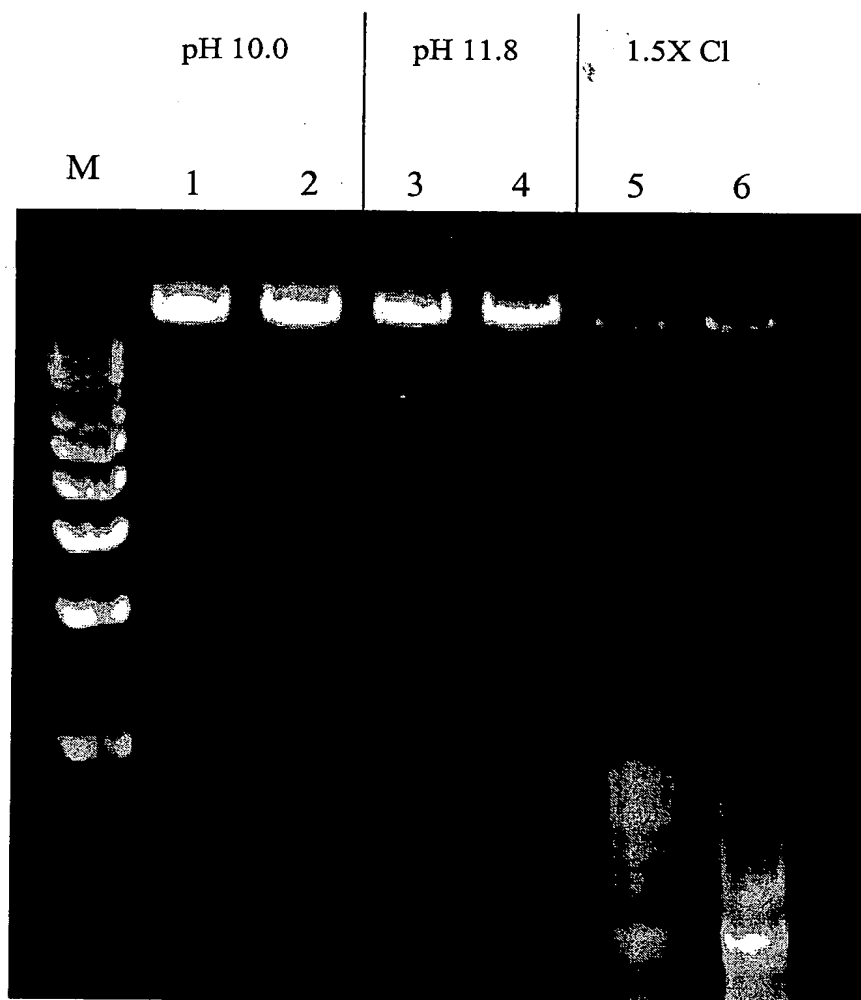
3/186

Fig. 4

19kb BG
30"/kb - 9.5' extension
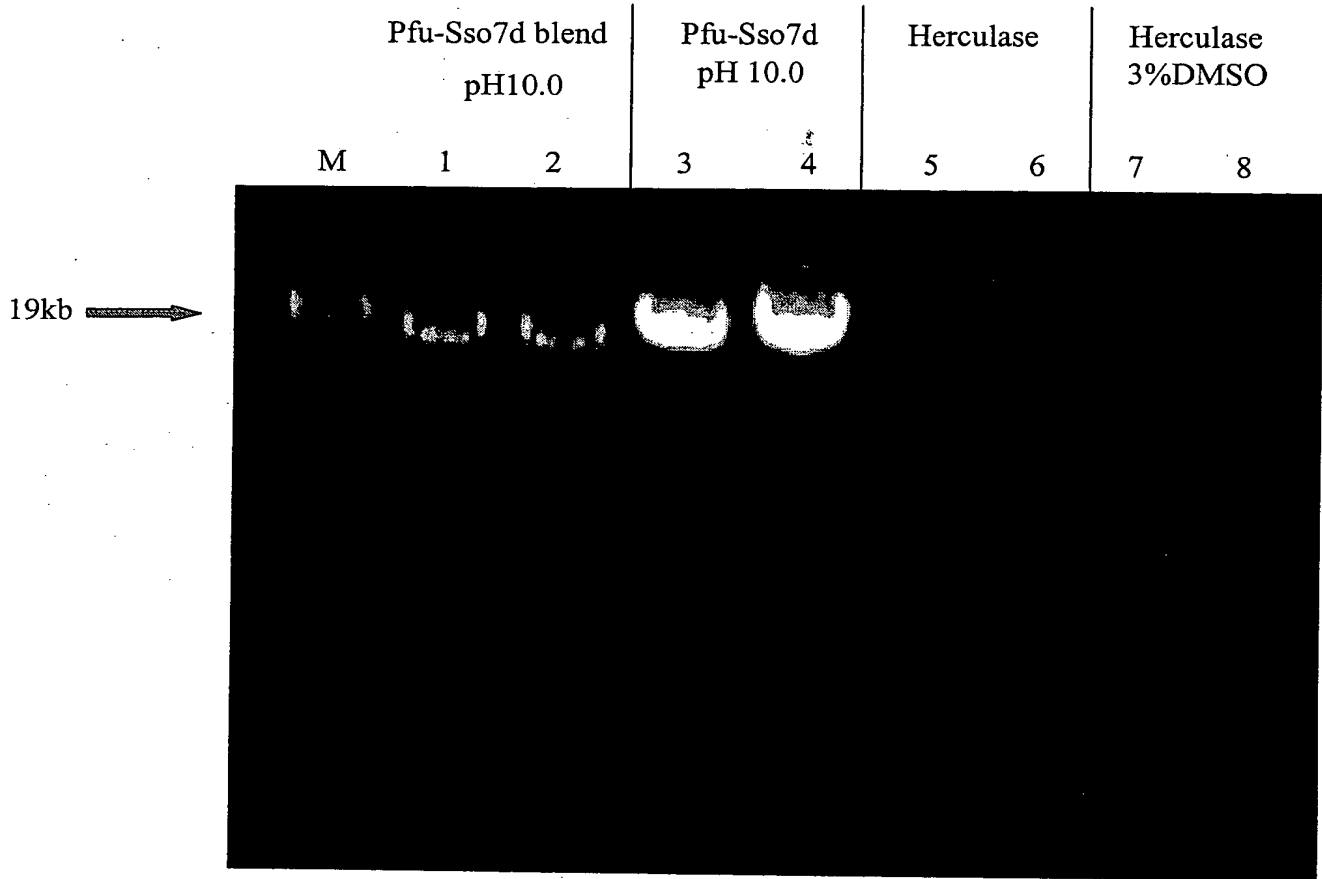
Fig. 5

19kb BG
30"/kb - 9.5' extension
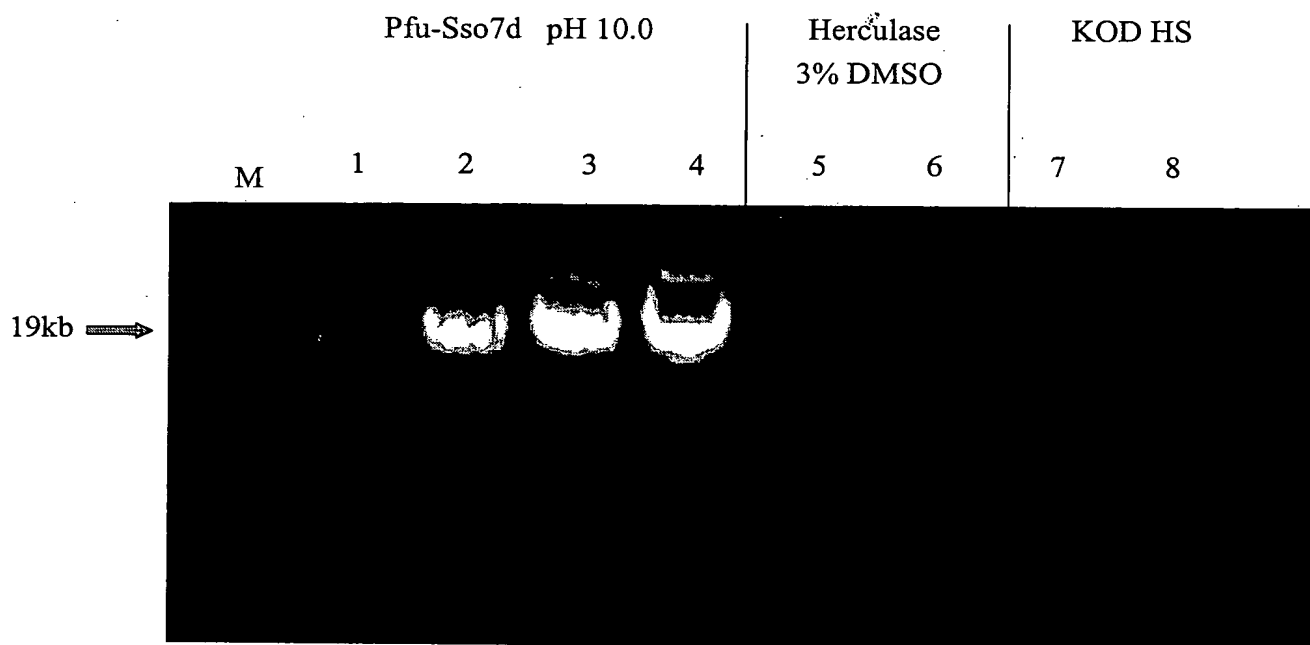
Pfu-Sso7d pH 10.0   Herculase   KOD HS
                            3% DMSO

M   1   2   3   4   5   6   7   8

19kb ⟹

Fig. 6

900bp HαAT
1"/kb – 1" extension

Fig. 7

**2.6kb HαAT
2"/kb - 5" extension**
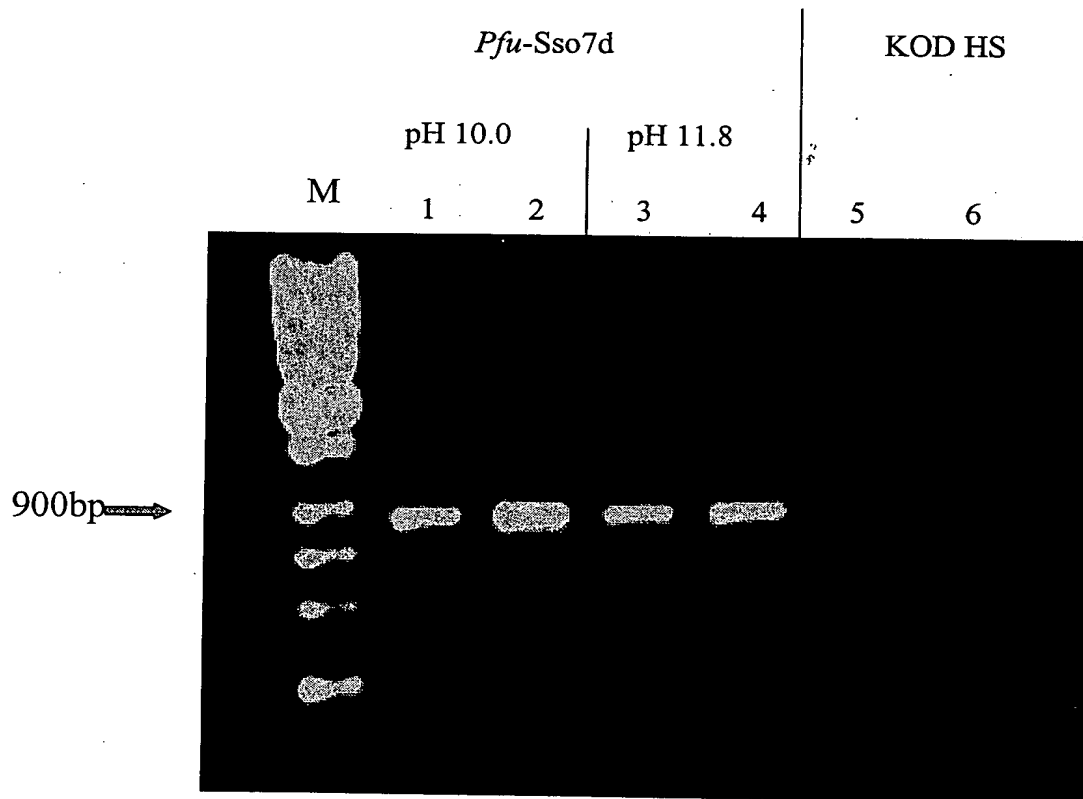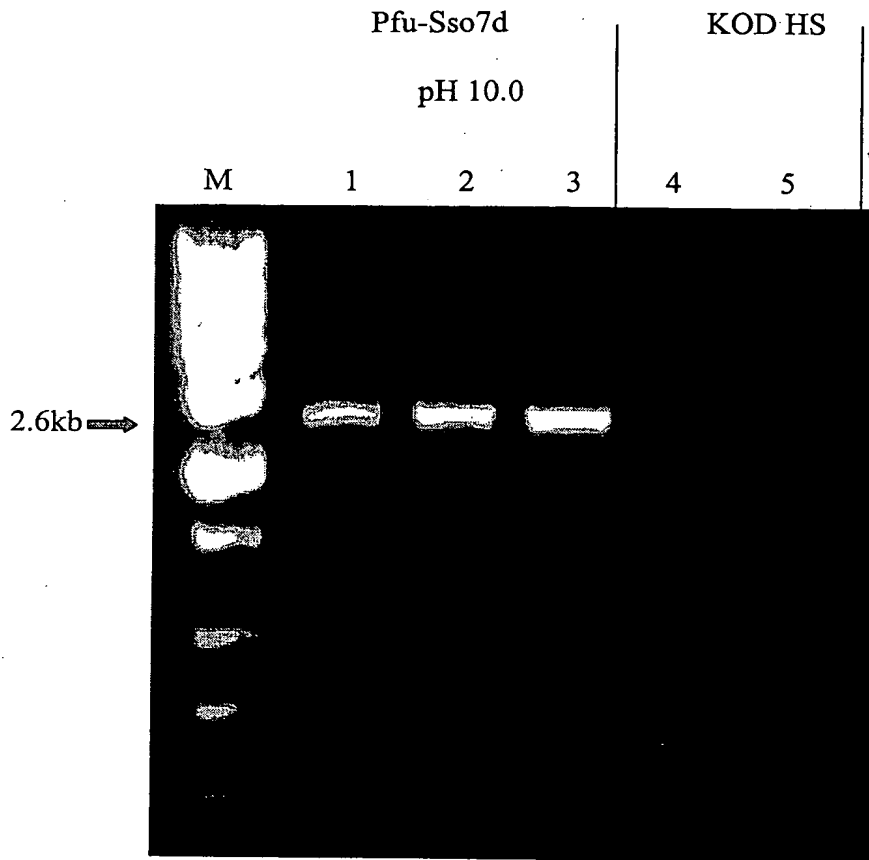
Fig. 8

6kb BG
10"/kb - 1' extension
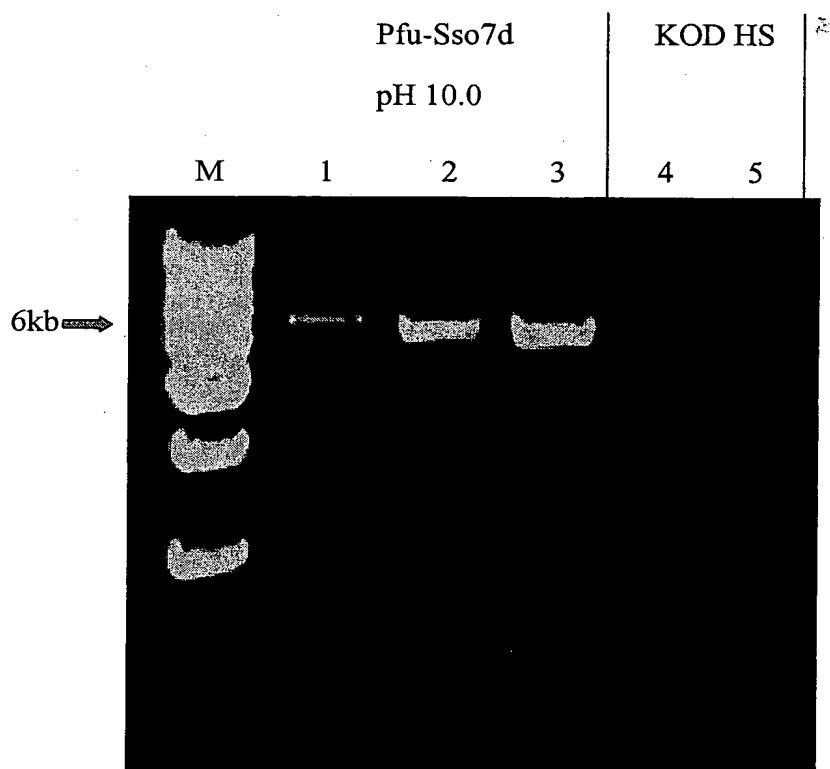
Fig. 9

2.6kb HαAT
30"/kb – 1'. 18" extension
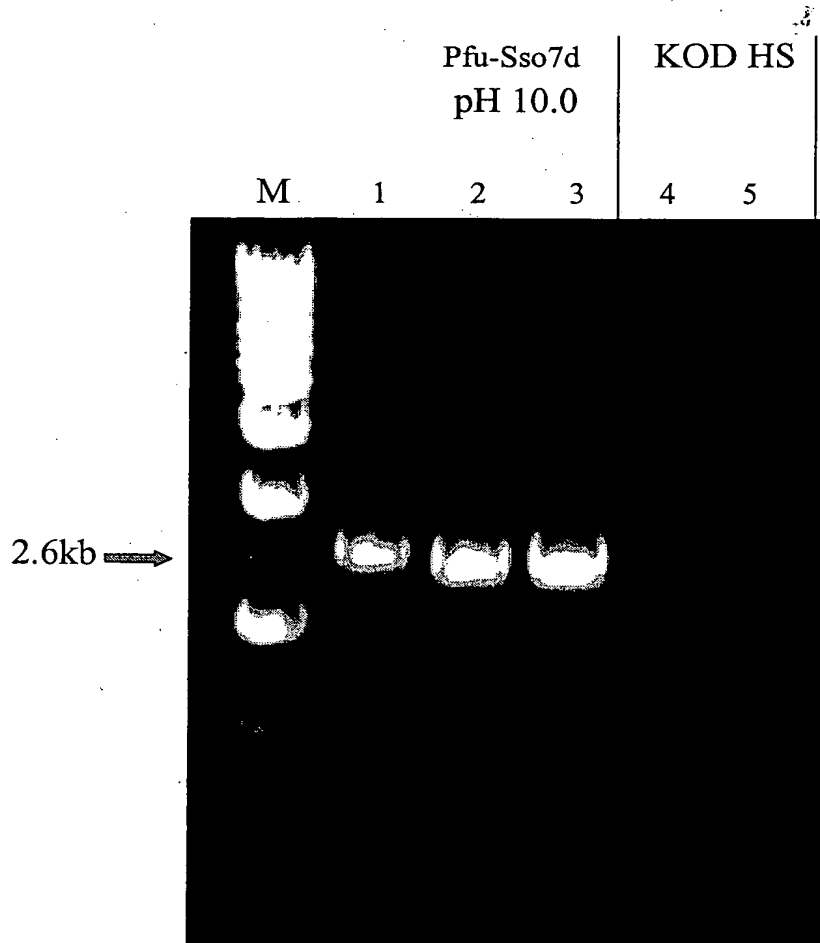
9|186

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATg<u>AA</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 6)

V93E#2

5'-CTTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 7)

V93R#1

5'-gAACATCCCCAAgAT<u>AgA</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 8)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 9)

V93N#1

5'-gAACATCCCCAAgAT<u>AAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 10)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 11)

V93H#1

5'-gAACATCCCCAAgAT<u>CAC</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 12)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 13)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgAT<u>NNK</u>CCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 14)

V93K#1

Fig. 10 (cont)

5'-gAACATCCCCAAgATAAACCCACTATTAgAg-3' (SEQ ID NO: 15)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 16)

QCM#1   5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAAg-(SEQ ID N 17)'

Alanine

QCM#2   5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID NO: 18)

Aspartic Acid

QCM#3   5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ I NO: 19)

Cysteine

QCM#4   5'-(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 20)

Isoleucine

QCM#5   5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 21)

Methionine

QCM#6   5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 22)

Phenylalanine

Fig 10 (con't)

QCM#7   5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Proline

QCM#8   5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9   5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID NO: 24)

Threonine

QCM#10   5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11   5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

a.)

200µM dUTP:

V93E		wt		V93R		V93R	
+	-	+	-	+	-	+	-

←2.3kb

b.)

V93R

dNTPs:	-	-	-	-	-	+	+
dUTP (µM):	400	200	100	50	0	200	0

←2.3kb

Figure 11

Figure 12

PFU DNA POLYMERASE
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```
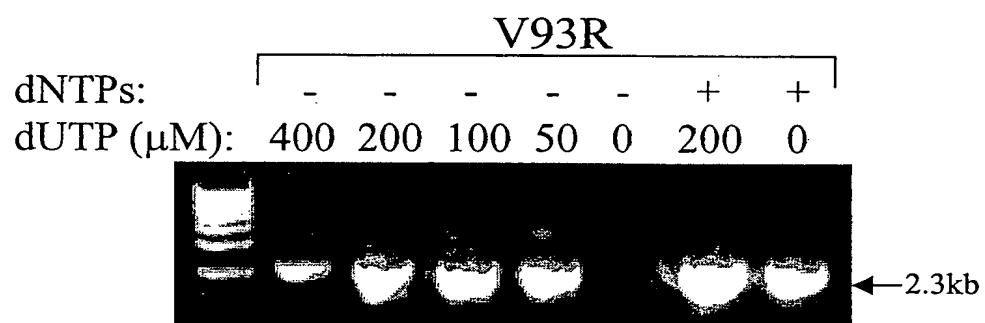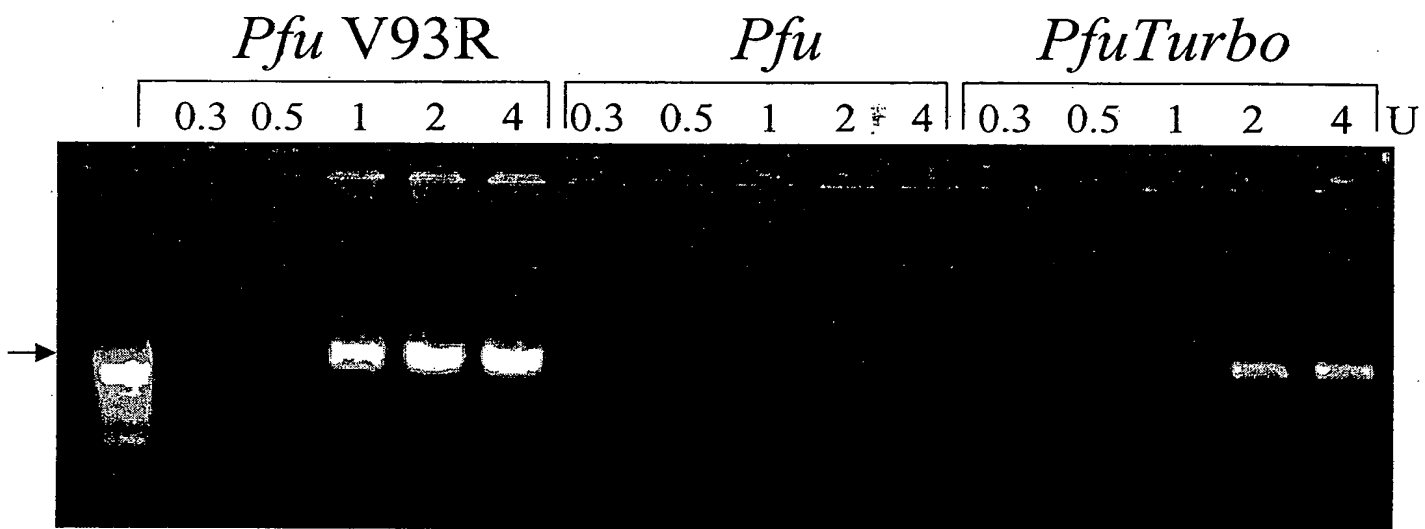
PFU DNA POLYMERASE
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
```

```
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

PFU DNA POLYMERASE
D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
```

```
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

KOD DNA POLYMERASE
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG AGAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA CTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG ACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
```

```
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CTTGA  2325
```

Vent DNA POLYMERASE
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT CTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGGTAG 2325
```

Deep Vent
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAACG  GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT    120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT    240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT    420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC    540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT    660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG    720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC    780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG    840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC    960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC    1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG    1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG    1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG    1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA    1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC    1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA    1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT    1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC    1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA    1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA    1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA    1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC    1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG    1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC    1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA    1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG    1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC    2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA    2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG    2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT    2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG    2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA               2328
```

JDF-3
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAGTTCCTCGGCAGGTCT
GTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGG
```

CGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCC
CAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAC CCT TCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGC GCC ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgcG
TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTC
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGG
GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/G387P

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI

LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK

Fig 13.B (con't)

KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK
ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK
ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Fig. 14-1

```
5' ATG ATC CTC GAT ACA GAC TAC ATA ACT GAG GAT GGA AAG CCC GTC ATC   48
   TAC TAG GAG CTA TGT CTG ATG TAT TGA CTC CTA CCT TTC GGG CAG TAG   48
    M   I   L   D   T   D   Y   I   T   E   D   G   K   P   V   I    16

   ACG ATC TTC AAG AAG GAG AAC GGC GAG TTC ACC ATA GAC TAC GAC AGA   96
   TGC TAG AAG TTC TTC CTC TTG CCG CTC AAG TGG TAT CTG ATG CTG TCT   96
    R   I   F   K   K   E   N   G   E   F   T   I   D   Y   D   R    32

   AAC TTT GAG CCA TAC ATC TAC GCG CTC TTG AAG GAC GAC TCT CCG ATT  144
   TTG AAA CTC GGT ATG TAG ATG CGC GAG AAC TTC CTG CTG AGA GGC TAA  144
    N   F   E   P   Y   I   Y   A   L   L   K   D   D   S   P   I    48

   GAG GAC GTC AAG AAG ATA ACT GCC GAG AGG CAC GGC ACT ACC GTT AGG  192
   CTC CTG CAG TTC TTC TAT TGA CGG CTC TCC GTG CCG TGA TGG CAA TCC  192
    E   D   V   K   K   I   T   A   E   R   H   G   T   T   V   R    64

   GTT GTC AGG GCC GAG AAA GTG AAG AAG AAG TTC CTA GGC AGC CCG ATA  240
   CAA CAG TCC CGG CTC TTT CAC TTC TTC TTC AAG GAT CCG TCC GGC TAT  240
    V   V   R   A   E   K   V   K   K   K   F   L   G   R   P   I    80

   GAG GTC TGG AAG CTC TAC TTC ACT CAC CCC CAG GAC NNN CCC GCA ATC  288
   CTC CAG ACC TTC GAG ATG AAG TGA GTG GGG GTC CTG     GGG CGT TAG  288
    E   V   W   K   L   Y   F   T   H   P   Q   D       P   A   I    96
```

Tgo 93   NNN = AGA, AGG, CGA, CGC, CGG, CGT   (R)
                GAA, GAG   (E)

25/186

Fig. 14-2

AGG GAC AAG ATA AAG GAG CAT CCT GCC GTT GTG GAC ATC TAC GAG TAC 336
TCC CTG TTC TAT TTC CTC GTA GGA CGG CAA CAC CTG TAG ATG CTC ATG 336
 R   D   K   I   K   E   H   P   A   V   V   D   I   Y   E   Y   112

GAC ATC CCC TTC GCG AAG CGC TAC CTC ATA GAC AAA GGC TTA ATC CCG 384
CTG TAG GGG AAG CGC TTC GCG ATG GAG TAT CTG TTT CCG AAT TAG GGC 384
 D   I   P   F   A   K   R   Y   L   I   D   K   G   L   I   P   128

ATG GAG GGC GAC GAG GAA CTT AAG ATG CTC GCC TTC GAC ATC GAG ACG 432
TAC CTC CCG CTG CTC CTT GAA TTC TAC GAG CGG AAG CTG TAG CTC TGC 432
 M   E   G   D   E   E   L   K   M   L   A   F   D   I   E   T   144

CTC TAT CAC GAG GGC GAG GAG TTC GCC GAA GGG CCT ATC CTG ATG ATA 480
GAG ATA GTG CTC CCG CTC CTC AAG CGG CTT CCC GGA TAG GAC TAC TAT 480
 L   Y   H   E   G   E   E   F   A   E   G   P   I   L   M   I   160

AGC TAC GCC GAC GAG GAA GGG GCG CGC GTT ATT ACC TGG AAG AAT ATC 528
TCG ATG CGG CTG CTC CTT CCC CGC GCG CAA TAA TGG ACC TTC TTA TAG 528
 S   Y   A   D   E   E   G   A   R   V   I   T   W   K   N   I   176

GAC CTT CCC TAT GTC GAC GTC GTT TCC ACC GAG AAG GAG ATG ATA AAG 576
CTG GAA GGG ATA CAG CTG CAG CAA AGG TGG CTC TTC CTC TAC TAT TTC 576
 D   L   P   Y   V   D   V   V   S   T   E   K   E   M   I   K   192

CGC TTC CTC AAG GTC GTC AAG GAA AAG GAT CCC GAC GTC CTC ATA ATC 624
GCG AAG GAG TTC CAG CAG TTC CTT TTC CTA GGG CTG CAG GAG TAT TAG 624
 R   F   L   K   V   V   K   E   K   D   P   D   V   L   I   I   208

Fig 14-3

```
TAC AAC GGC GAC AAC TTC GAC TTC GCC TAC CTC AAG AAG CGC TCC GAG   672
ATG TTG CCG CTG TTG AAG CTG AAG CGG ATG GAG TTC TTC GCG AGG CTC   672
 Y   N   G   D   N   F   D   F   A   Y   L   K   K   R   S   E    224

AAG CTC GGA GTC AAG TTC ATC CTC GGA AGG GAA GGG AGC GAA CCG AAA   720
TTC GAG CCT CAG TTC AAG TAG GAG CCT TCC CTT CCC TCG CTT GGC TTT   720
 K   L   G   V   K   F   I   L   G   R   E   G   S   E   P   K    240

ATC CAG CGC ATG GGC GAT CGC TTT GCG GTG GAG GTC AAG GGA AGG ATT   768
TAG GTC GCG TAC CCG CTA GCG AAA CGC CAC CTC CAG TTC CCT TCC TAA   768
 I   Q   R   M   G   D   R   F   A   V   E   V   K   G   R   I    256

CAC TTC GAC CTC TAC CCC GTC ATT AGG AGA ACG ATT AAC CTC CCC ACT   816
GTG AAG CTG GAG ATG GGG CAG TAA TCC TCT TGC TAA TTG GAG GGG TGA   816
 H   F   D   L   Y   P   V   I   R   R   T   I   N   L   P   T    272

TAC ACC CTT GAG GCA GTA TAT GAA GCC ATC TTT GGA CAG CCG AAG GAG   864
ATG TGG GAA CTC CGT CAT ATA CTT CGG TAG AAA CCT GTC GGC TTC CTC   864
 Y   T   L   E   A   V   Y   E   A   I   F   G   Q   P   K   E    288

AAG GTC TAC GCT GAG GAG ATA GCG CAG GCC TGG GAA ACG GGC GAG GGA   912
TTC CAG ATG CGA CTC CTC TAT CGC GTC CGG ACC CTT TGC CCG CTC CCT   912
 K   V   Y   A   E   E   I   A   Q   A   W   E   T   G   E   G    304

TTA GAA AGG GTG GCC CGC TAC TCG ATG GAG GAC GCG AAG GTA ACC TAT   960
AAT CTT TCC CAC CGG GCG ATG AGC TAC CTC CTG CGC TTC CAT TGG ATA   960
 L   E   R   V   A   R   Y   S   M   E   D   A   K   V   T   Y    320
```

Fig 14-4

```
GAA CTC GGA AAA GAG TTC TTC CCT ATG GAA CCC CAG CTC TCG CGC CTC  1008
CTT GAG CCT TTT CTC AAG AAG GGA TAC CTT CGG GTC GAG AGC GCG GAG  1008
 E   L   G   K   E   F   F   P   M   E   A   Q   L   S   R   L   336

GTA GGC CAG AGC CTC TGG GAT GTA TCT CGC TCG AGT ACC GGA AAC CTC  1056
CAT CCG GTC TCG GAG ACC CTA CAT AGA GCG AGC TCA TGG CCT TTG GAG  1056
 V   G   Q   S   L   W   D   V   S   R   S   S   T   G   N   L   352

GTC GAG TGG TTT TTG CTG AGG AAG GCC TAC GAG AGG AAT GAA CTT GCA  1104
CAG CTC ACC AAA AAC GAC TCC TTC CGG ATG CTC TCC TTA CTT GAA CGT  1104
 V   E   W   F   L   L   R   K   A   Y   E   R   N   E   L   A   368

CCA AAC AAG CCG GAC GAG AGG GAG CTG GCA AGA AGA AGG GAG AGC TAC  1152
GGT TTG TTC GGC CTG CTC TCC CTC GAC CGT TCT TCT TCC CTC TCG ATG  1152
 P   N   K   P   D   E   R   E   L   A   R   R   R   E   S   Y   384

GCG GGT GGA TAC GTC AAG GAG CCC GAA AGG GGA CTG TGG GAG AAC ATC  1200
CGC CCA CCT ATG CAG TTC CTC GGG CTT TCC CCT GAC ACC CTC TTG TAG  1200
 A   G   G   Y   V   K   E   P   E   R   G   L   W   E   N   I   400

GTG TAT CTG GAC TTC CGC TCC CTG TAT CCT TCG ATA ATA ATC ACC CAT  1248
CAC ATA GAC CTG AAG GCG AGG GAC ATA GGA AGC TAT TAT TAG TGG GTA  1248
 V   Y   L   D   F   R   S   L   Y   P   S   I   I   I   T   H   416

AAC GTC TCC CCT GAT ACA CTC AAC AGG GAG GGT TGT GAG GAG TAC GAC  1296
TTG CAG AGG GGA CTA TGT GAG TTG TCC CTC CCA ACA CTC CTC ATG CTG  1296
 N   V   S   P   D   T   L   N   R   E   G   C   E   E   Y   D   432
```

28/186

Fig. 14-5

```
GTG GCT CCT CAG GTA GGC CAT AAG TTC TGC AAG GAC TTC CCC GGC TTC   1344
CAC CGA GGA GTC CAT CCG GTA TTC AAG ACG TTC CTG AAG GGG CCG AAG   1344
 V   A   P   Q   V   G   H   K   F   C   K   D   F   P   G   F    448

ATC CGA AGC CTC CTC GGA GAC CTC TTG GAG GAG AGA CAG AAG GTA AAG   1392
TAG GGT TCG GAG GAG CCT CTG GAG AAC CTC CTC TCT GTC TTC CAT TTC   1392
 I   P   S   L   L   G   D   L   L   E   E   R   Q   K   V   K    464

AAG AAG ATG AAG GCC ACT ATA GAC CCA ATC GAG AAG AAA CTC CTC GAT   1440
TTC TTC TAC TTC CGG TGA TAT CTG GGT TAG CTC TTC TTT GAG GAG CTA   1440
 K   K   M   K   A   T   I   D   P   I   E   K   K   L   L   D    480

TAC AGG CAA CGA CCA ATC AAA ATC CTT GCT AAT AGC TTC TAC GGT TAC   1488
ATG TCC GTT GCT CGT TAG TTT TAG GAA CGA TTA TCG AAG ATG CCA ATG   1488
 Y   R   Q   R   A   I   K   I   L   A   N   S   F   Y   G   Y    496

TAC GGC TAT ACA AAG GCC CGC TGG TAC TAC AAG GAG TGC GCC GAG AGC   1536
ATG CCG ATA TGT TTC CGG GCG ACC ATG ATG TTC CTC ACG CGG CTC TCG   1536
 Y   G   Y   T   K   A   R   W   Y   Y   K   E   C   A   E   S    512

GTT ACC GGT TGG GCC AGG GAG TAC ATC GAG ACC ACG ATA AGG GAA ATA   1584
CAA TGG CCA ACC CGG TCC CTC ATG TAG CTC TGG TGC TAT TCC CTT TAT   1584
 V   T   G   W   G   R   E   Y   I   E   T   T   I   R   E   I    528

GAG GAG AAA TTT GGC TTT AAA GTC CTC TAC GCG GAC ACA GAT GGA TTT   1632
CTC CTC TTT AAA CCG AAA TTT CAG GAG ATG CGC CTG TGT CTA CCT AAA   1632
 E   E   K   F   G   F   K   V   L   Y   A   D   T   D   G   F    544

TTC GCA ACA ATA CCT GGA GCG GAC GCC GAA ACC GTC AAA AAG AAG GCA   1680
AAG CGT TGT TAT GGA CCT CGC CTG CGG CTT TGG CAG TTT TTC TTC CGT   1680
 F   A   T   I   P   G   A   D   A   E   T   V   K   K   K   A    560
```

Fig 14-6

```
AAG GAG TTC CTG GAC TAC ATC AAC GCC AAA CTG CCC GGC CTG CTC GAA   1728
TTC CTC AAG GAC CTG ATG TAG TTG CGG TTT GAC GGG CCG GAC GAG CTT   1728
  K   E   F   L   D   Y   I   N   A   K   L   P   G   L   L   E   576
```

```
CTC GAA TAC GAG CGC TTC TAC AAG CGC GGC TTC TTC GTG ACG AAG AAG   1776
GAG CTT ATG CTC GCG AAG ATG TTC GCG CCG AAG AAG CAC TGC TTC TTC   1776
  L   E   Y   E   G   F   Y   K   R   G   F   F   V   T   K   K   592
```

```
AAG TAC GCG GTT ATA GAC GAG GAG GAC AAG ATA ACG ACG CGC GGG CTT   1824
TTC ATG CGC CAA TAT CTG CTC CTC CTG TTC TAT TGC TGC GCG CCC GAA   1824
  K   Y   A   V   I   D   E   E   D   K   I   T   T   R   G   L   608
```

```
GAA ATA GTT AGG CGT GAC TGG AGC GAG ATA GCG AAG GAG ACG CAG GCG   1872
CTT TAT CAA TCC GCA CTG ACC TCG CTC TAT CGC TTC CTC TGC GTC CGC   1872
  E   I   V   R   R   D   W   S   E   I   A   K   E   T   Q   A   624
```

```
AGG GTT CTT GAG GCG ATA CTA AAG CAC GGT GAG GTT GAA GAA GCG GTA   1920
TCC CAA GAA CTC CGC TAT GAT TTC GTG CCA CTG CAA CTT CTT CGC CAT   1920
  R   V   L   E   A   I   L   K   H   G   D   V   E   E   A   V   640
```

```
AGG ATT GTC AAA CAG GTT ACG GAG AAG CTG AGC AAG TAC GAG GTT CCA   1968
TCC TAA CAG TTT CTC CAA TGC CTC TTC GAC TCG TTC ATG CTC CAA GGT   1968
  R   I   V   K   E   V   T   E   K   L   S   K   Y   E   V   P   656
```

```
CCG GAG AAG CTG GTC ATC TAC GAG CAG ATA ACC CGC GAC CTG AAG GAC   2016
GGC CTC TTC GAC CAG TAG ATG CTC GTC TAT TGG GCG CTG GAC TTC CTG   2016
  P   E   K   L   V   I   Y   E   Q   I   T   R   D   L   K   D   672
```

Fig. 14-7

```
TAC AAG GCC ACC GGG CCG CAT GTG GCT GTT GCA AAA CGC CTC GCC GCA   2064
ATG TTC CGG TGG CCC GGC GTA CAC CGA CAA CGT TTT GCG GAG CGG CGT   2064
 Y   K   A   T   G   P   H   V   A   V   A   K   R   L   A   A    688

AGG GGG ATA AAA ATC CGG CCC GGA ACG GTC ATA AGC TAC ATC GTG CTC   2112
TCC CCC TAT TTT TAG GCC GGG CCT TGC CAG TAT TCG ATG TAG CAC GAG   2112
 R   G   I   K   I   R   P   G   T   V   I   S   Y   I   V   L    704

AAA GGC TCG GGA AGG ATT GGG GAC AGG GCT ATA CCC TTT GAC GAA TTT   2160
TTT CCG AGC CCT TCC TAA CCC CTG TCC CGA TAT GGG AAA CTG CTT AAA   2160
 K   G   S   G   R   I   G   D   R   A   I   P   F   D   E   F    720

GAC CCG GCA AAG CAC AAG TAC GAT GCA GAA TAC TAC ATC GAG AAC CAG   2208
CTG GGC CGT TTC GTG TTC ATG CTA CGT CTT ATG ATG TAG CTC TTG GTC   2208
 D   P   A   K   H   K   Y   D   A   E   Y   Y   I   E   N   Q    736

GTT CTT CCA GCT GTG GAG AGG ATT CTG AGG GCC TTT GGT TAC CGT AAA   2256
CAA GAA GGT CGA CAC CTC TCC TAA GAC TCC CGG AAA CCA ATG GCA TTT   2256
 V   L   P   A   V   E   R   I   L   R   A   F   G   Y   R   K    752

GAA GAT TTA AGG TAT CAG AAA ACG CGG CAG GTT GGC TTG GGG CCG TGG   2304
CTT CTA AAT TCC ATA GTC TTT TGC GCC GTC CAA CCG AAC CCC CGC ACC   2304
 E   D   L   R   Y   Q   K   T   R   Q   V   G   L   G   A   W    768

CTA AAA CCT AAG ACA TGA                                           2322
GAT TTT GGA TTC TGT ACT                                           2322
 L   K   P   K   T   *                                            773
```
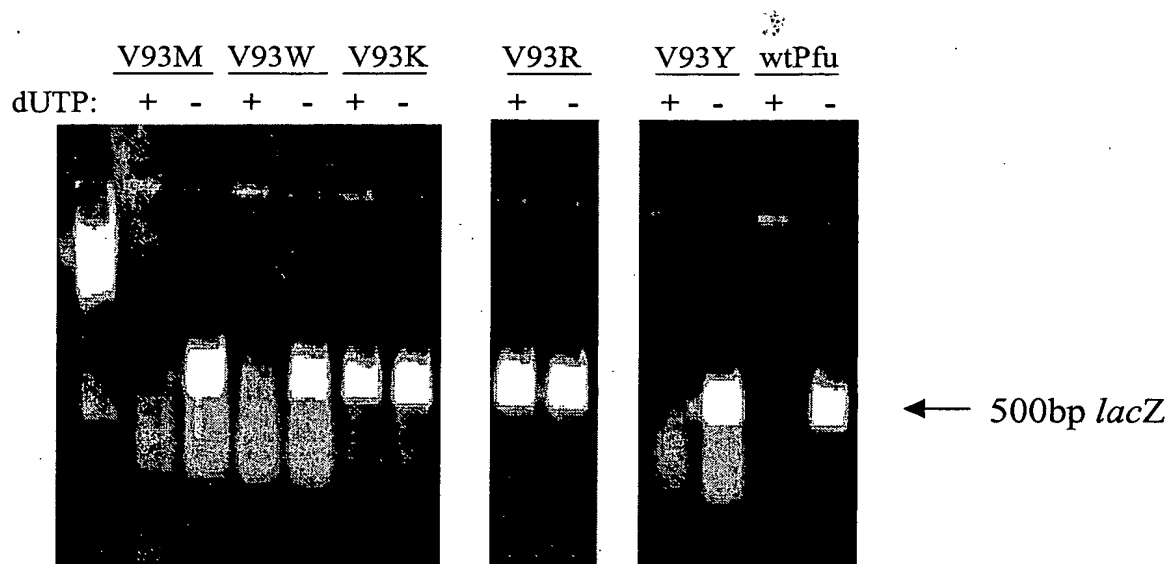
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

Figure 15A
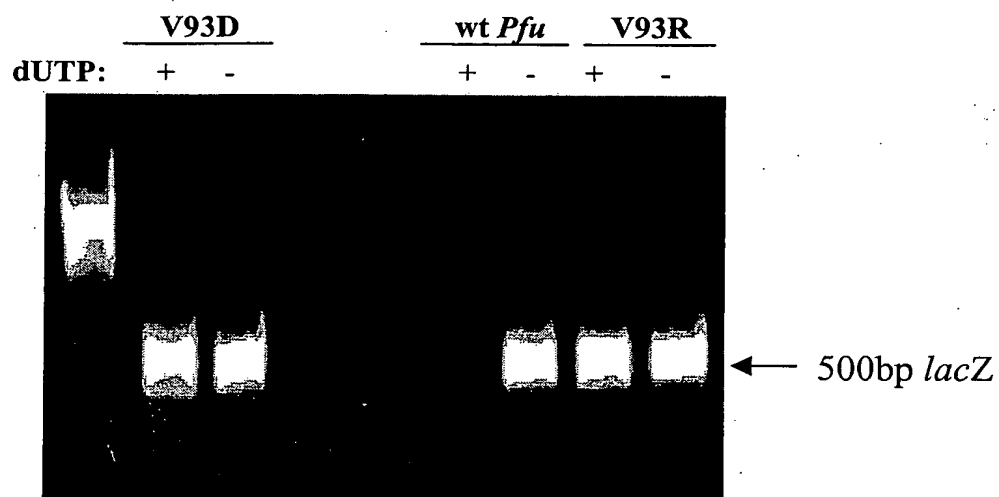
Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

Figure 15B

wt *Pfu* 1   wt *Pfu* 2   V93G (.5μl) V93G (2 μl) V93N (.5μl) V93N (2 μl)

400 200   0 400 200   0 400 200   0 400 200   0 400 200   0 400 200   0μM dUTP

← 500bp *lacZ*
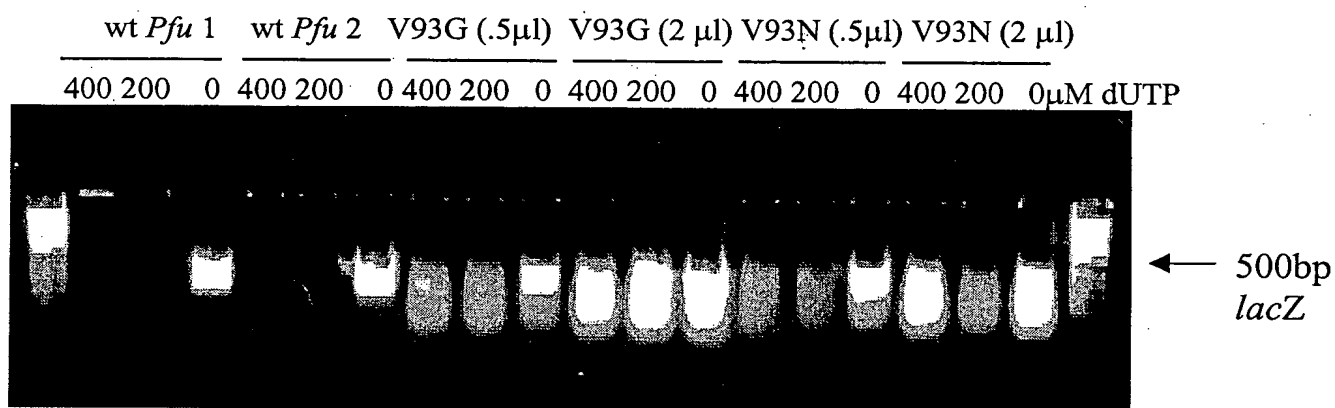
Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 15C

34|186

Figure 16:   Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Pyrococcus furiosus gene for archaeal histone (HMf-like) (Fig. 17-A)
(ACCESSION No: AB013081)

```
M   M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G          18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54

A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E          36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA     108

K   A   I   E   I   A   K   A   V   D   L   A   K   H   A   G   R              54
AAA GCT ATT GAG ATC GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA         162

K   T   V   K   V   E   D   I   K   L   A   I   K   S   *                      69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA                  207
```

(HMf-like)-Taq DNA polymerase fusion protein (Fig.17-B)

```
M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G              18
ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT          54

A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E          36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA     108

K   A   I   E   I   A   K   A   V   D   L   A   K   H   A   G   R              54
AAA GCT ATT GAG ATC GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA         162

K   T   V   K   V   E   D   I   K   L   A   I   K   S                          69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC

                                    G   G   G
//                                  GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
```

Fig. 17B (cont')

```
D    G    H    H    L    A    Y    R    T    F    H    A    L    K    G    L    T    T
GAC  GGC  CAC  CAC  CTG  GCC  TAC  CGC  ACC  TTC  CAC  GCC  CTG  AAG  GGC  CTC  ACC  ACC

S    R    G    E    P    V    Q    A    X    Y    G    F    A    K    S    L    L    K
AGC  CGG  GGG  GAG  CCG  GTG  CAG  GCG  OTC  TAC  GGC  TTC  GCC  AAG  AGC  CTC  CTC  AAG

A    L    K    E    D    G    D    A    V    I    V    V    F    D    A    K    A    P
GCC  CTC  AAG  GAG  GAC  GGG  GAC  GCG  GTG  ATC  GTG  GTG  TTT  GAC  GCC  AAG  GCC  CCC

S    F    R    H    E    A    Y    G    G    Y    K    A    G    R    A    P    T    P
TCC  TTC  CGC  CAC  GAG  GCA  TAC  GGG  GGG  TAC  AAG  GCG  GGC  CGG  GCC  CCC  ACG  CCA

E    D    F    P    R    Q    L    A    L    I    K    E    L    V    D    L    L    G
GAG  GAC  TTT  CCC  CGG  CAA  CTC  GCC  CTC  ATC  AAG  GAG  CTG  GTG  GAC  CTG  CTG  GGG

L    A    R    L    E    V    P    G    Y    E    A    D    D    V    L    A    S    L
CTG  GCG  CGC  CTC  GAG  GTC  CCG  GGC  TAC  GAG  GCG  GAC  GAC  GTC  CTG  GCC  AGC  CTG

A    K    A    E    K    E    G    Y    E    V    R    I    L    T    A    D    K
GCC  AAG  GCG  GAA  AAG  GAG  GGC  TAC  GAG  GTC  CGC  ATC  CTC  ACC  GCC  GAC  AAA

D    L    Y    Q    L    S    D    R    I    H    V    L    H    P    E    G    Y
GAC  CTT  TAC  CAG  CTT  TCC  GAC  CGC  ATC  CAC  GTC  CTC  CAC  CCC  GAG  GGG  TAC

L    I    T    P    A    W    L    W    E    K    Y    G    L    R    P    D    Q    W
CTC  ATC  ACC  CCG  GCC  TGG  CTT  TGG  GAA  AAG  TAC  GGC  CTG  AGG  CCC  GAC  CAG  TGG

A    D    Y    R    A    L    T    G    D    E    S    D    N    L    P    G    V    K
GCC  GAC  TAC  CGG  GCC  CTG  ACC  GGG  GAC  GAG  TCC  GAC  AAC  CTT  CCC  GGG  GTC  AAG

G    I    G    E    K    T    A    R    K    L    L    E    E    W    G    S    L    E
GGC  ATC  GGG  GAG  AAG  ACG  GCG  AGG  AAG  CTT  CTG  GAG  TGG  GGG  AGC  CTG  GAA

A    L    L    K    N    L    D    R    L    K    P    A    I    R    E    K    I    L
GCC  CTC  AAG  AAC  CTG  GAC  CGG  CTG  AAG  CCC  GCC  ATC  CGG  GAG  AAG  ATC  CTG

A    H    M    D    D    L    K    L    S    W    D    L    A    K    V    R    T    D
GCC  CAC  ATG  GAC  GAT  CTG  AAG  CTC  TCC  TGG  GAC  CTG  GCC  AAG  GTG  CGC  ACC  GAC
```

```
L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   S   L   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   A   P   W   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
CTG GCC GCC AGG GGG CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L   R   D   L   K   E   A   G   L   L   P   E   G   V   A   R   R   Y   G
CTC AGG GAC CTG AAG GAG GCC GGC CTT CCG GAG GTG GCC CGG CGC TAC GGC

G   E   W   T   E   A   G   E   R   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCA GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

Y   L   L   D   P   S   N   T   T   P   E   G   D   D   P   M   L   L   A
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGC GAC GAC CCC ATG CTC CTG GCC

A   N   L   W   G   R   L   E   G   E   E   R   A   A   L
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG CGG GCC GCC CTT

E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A   R   L   E   A   E   V   F   R   L   A   G   H   P   F   N   L   N
GCC CGC CTC GAG GAG GTC TTC CGC CTG GCC GGG CAC CCC TTC AAC CTC AAC
```

38/186

```
S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   L   Q   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC CTG CAG AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   A   I   H   P   R   T
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ATC CAC CCC AGG ACG

S   S   D   P   N   L   Q   N   I   P   V   R   L   G   Q   R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC CTT GGG CAG AGG

I   R   R   A   F   I   A   E   E   G   W   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S   Q   I   E   L   R   V   L   A   H   L   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R   V   F   Q   E   G   R   D   I   H   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG AGC TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG CGG GCG AAG ACC ATC

N   F   G   V   L   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGG CTC TCC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   G   Y
AAG GTC CGA GCC TGG ATC GAG AAG ACC CTG GAG GAG GGC CGG CGG GGA TAC CCC
```

39/186

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V   E   T   L   F   G   R   R   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCC GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

L   S   A   K   E   G   I   D   G   R   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

H   H   *
CAT CAT TAA

Taq DNA polymerase- (HMf-like) fusion protein (Fig. 17-C)

G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T

Fig 17C (con't)

GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG TAC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTC ATC GTG TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGG CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG TGG GGG AGC CTG GAA

A   L   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

41/186

```
L    P    L    E    V    D    F    A    K    R    R    E    P    D    R    E    R    L
CTG  CCC  CTG  GAG  GTG  GAC  TTC  GCC  AAA  AGG  CGG  GAG  CCC  GAC  CGG  GAG  AGG  CTT

R    A    F    L    E    R    L    E    E    F    G    S    L    H    E    F    G    L
AGG  GCC  TTT  CTG  GAG  AGG  CTT  GAG  GAG  TTT  GGC  AGC  CTC  CAC  GAG  TTC  GGC  CTT

L    E    S    P    K    A    L    E    E    A    P    E    G    A
CTG  GAA  AGC  CCC  AAG  GCC  CTG  GAG  GAG  GCC  CCG  GAA  GGG  GCC

F    V    G    F    V    L    S    R    K    E    P    M    W    A    D    L    L    A
TTC  GTG  GGC  TTT  GTG  CTT  TCC  CGC  AAG  GAG  CCC  ATG  TGG  GCC  GAT  CTT  CTG  GCC

L    A    A    R    G    G    R    V    H    R    A    P    M    W    A    P    Y    K    A
CTG  GCC  GCC  AGG,GGG  GGC  GGC  CGG  GTC  CAC  CGG  GCC  CCC  ATG  TGG  GCC  CCT  TAT  AAA  GCC

L    R    E    G    L    K    E    A    L    S    V    L
CTC  AGG  GAG  GGC  CTT  AAG  GAG  GCG  CTC  AGC  GTT  CTG

Y    L    D    P    S    N    T    T    P    E    G    D    D    P    M    L    L    A
TAC  CTC  GAC  CCT  TCC  AAC  ACC  ACC  CCG  GAG  GGT  GAC  GAC  CCC  ATG  CTC  CTC  GGC

A    L    R    E    G    L    P    P    G    V    A    R    R    Y    G
GCC  CTG  AGG  GAA  GGC  CTT  CCG  GGG  GTG  GAC  GAC  CGG  CGC  TAC  GGC

G    E    W    T    E    A    G    E    R    A    A    L    S    E    R    L    F
GGG  GAG  TGG  ACG  GAG  GAG  GCG  CGG  GAG  GCC  GTG  GCC  CTT  TCC  GAG  AGG  CTC  TTC

A    N    L    W    G    R    L    E    G    E    R    L    W    L    Y    R
GCC  AAC  CTG  TGG  GGG  AGG  CTT  GAG  GGG  GAG  CGG  CTC  CTT  TGG  CTT  TAC  CGG

G    E    R    P    L    S    A    V    L    A    H    M    E    A    T    G    V
GAG  GAG  AGG  CCC  CTT  GCT  GTC  GCC  CAC  ATG  GAG  GCC  ACG  GGG  GTG

E    V    E    R    P    L    S    A    V    L    E    G    E    E    I
GAG  GTG  GAG  AGG  CCC  CTT  TCC  GCT  GTC  CTG  GAG  GGG  GAG  GAG  ATC

R    L    D    V    A    Y    L    R    A    S    L    E    V    A    E    V
CGC  CTG  GAC  GTG  GCC  TAT  CTC  AGG  GCC  TTG  TCC  CTG  GAG  GTG  GCC  GAG  GTG

A    R    L    E    A    E    V    F    R    L    A    G    H    P    F    N    L    N
GCC  CGC  CTC  GAG  GAG  GTC  TTC  CGC  CTG  GCC  GGC  CAC  CCC  TTC  AAC  CTC  AAC
```

42/186

```
S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGG AAG CGC TCC ACC AGC GCC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   P   L   G   R   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG CCG CTT GGG CAG AGT

S   D   P   N   L   Q   N   I   P   V   R   A   T   I   H   D   Y
AGC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC GCC ACC ATC CAC GAC TAT

I   R   R   A   F   I   A   E   E   G   W   L   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S   Q   I   E   L   R   V   L   A   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC TCC GGC GAC GAG AAC CTG ATC

R   V   F   Q   E   G   R   D   I   H   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC GAG ACC GCG TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG CGG GCG AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGG CTC TCC CAG GAG CTA

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
AAG GTC CGA GCC TGG ATC GAG AAG ACC CTG GAG GAG GGC CGG CGG GGC
```

43/186

```
K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V   E   T   L   F   G   R   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   E   R   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCC GCC GAG CGC AAC ATG CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCG ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC ATG CTC CTT CAG GTC CAC GAC GAG CTC GTC CTG GAG GCC

P   K   E   R   A   E   A   V   A   R   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GGG ATA GGG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG ATT GAT GGC CGC GGA GGG GGG CAT CAT CAT

H   H   //
CAT CAT   //

M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G
ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT

A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E
GCT CAG AGA GTT AGC GAA CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA

K   I   E   I   A   K   A   V   D   L   A   K   H   A   G   R
AAA ATT GAG ATC GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA

K   T   V   K   V   E   D   I   K   L   A   I   K   S   *
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

18
54
36
108
54
162
69

Pfu DNA Polymerase (WT) -(HMf-like) fusion protein (Fig. 17-D)

//

ccctggtcct gggtccacat atatgtttctt actcgccttt atgaagaatc cccagtcgc

tctaaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaaagaga acggaaaatt

taagatagag catgatataga ctttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccggtgt ggaaacttta

tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaacccctta

tcacgaagga gaagagttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag

cgagagagag atgatataaga gattatcaag gagaaggatc ctgacattat

agttacttat aatggagact cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccaatg gaagagatgg aagcgagccca aagatgcaga gaataggcga

tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag

gacaaataat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtataacgcc acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagtttgcc aaatactcga tggaagatgc aaaggcaaact tatgaactcg ggaaagaatt

ccttccaatg gaaattcaag tttcaagatt agttggacaa cccttatggg atgtttcaag

gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

agtagctcca aacaagccaa gtgaagaaga gtatcaaaga aggctcaggg agagctacac

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt

tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

tgaggggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat

aaaaatgaag gaaactcaag atccctataga aaaaatactc cttgactata gacaaaaagc

ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac

gataaaactc ttagcaaatt cttctacgg atattatggc tatgcaaaag caagatggta

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

gaaggagctc gaagaaaagt ttggatttaa agtccctcac attgacactg atggtctccta

tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag

gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaagaa aagtcattac

tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag

agtttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga

Fig 17D (cont)

```
agtaatacaa aagcttgcca attatgaaat tccaccaag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggccgatggt ccaattagca ataggccaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac attttctaact ttgcaactct
tcaagatttt ctaaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctaacct
tttgtctcaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
ttccgggagt tttgtattgc tctagccaag gttttgggatt tttgaatcct ttaactctgg
taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tcttctcatag aggagggnnn nngtcctctc
```

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg //

<u>(HMf-like) - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-E)</u>

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat

caactctaca cctccctat tttctctctt atgagatttt taagtatagt tatagagaag

gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

aaagagttaaga aaataacggg ggaaaaggcat ggaaagattg tgagaattgt

```
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaactta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgatataaaga gattctcaag gattatcaag gagaagatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaatagccga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaatt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gttgaagagga gtatcaaaga aggctcaggg agagctacac
agttggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgaaggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
```

Fig. 17E (cont)

```
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agtttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccagcggtac ttaggatatt
ggaggggatt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcctc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
```

50|186

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaattttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg

aaagtatat ttcaagctcc ttcttcttca tgacagatga aaaattgtt tgtctctttt

taactttta agaaataact gttctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tcttttcatag aggaggnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtggggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg   //   TGA

(HMf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein (Fig. 17-F)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG ATC GCA AAG AAG GCA GAT CTT GCA GAT CTC GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
```

//ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCTT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACGGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAC GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG AAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAG GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGGAGA GCTACACAGG
TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGAATTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGGTACTG TAAGGAGTGT GCTGAGACG TTACTGCTGG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACCTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTTGGAGACA ATACTAAAAC ACGGAGAGATGT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980 CTCGCAAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACAATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAG GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
                                                                          2328
```

// TGA

PFU DNA POLYMERASE (V93 R OR E)-(HMf-like) fusion protein (Fig. 17-G)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGTCT 120 CTTCTCAGGG ATGATTATTAG GTTAAGAAGA GTTAAGAAAA TAACGGGGGA AAGGCAATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAGA AGTTTCTCGG CAAGCCTATT 240 ACGGTGTTGGA AACTTTTATTT GGAACATTCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGATAT GACGGCTGTTA GAAGTCAAGG GAAGAAATACA TTTCGACTTG 780 TATCAATGTAA TAACAAGGAC AATAAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTTCTT ACTTAGGGAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGGAGA GCTACACAGG
TGGATTCGTT AAAGAGCCAG AAAAAGGGGGTT GTGGGAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA 1260 AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA TCTACGGATA TTAIATGGCTAT 1500
GCAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGGAGCTCGAA
GAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATTAT 1740 GAAGGGTTTT ATAAGAGGG
ATTCTTCGTT ACGAAGAAGA GGTAGCGTCAGT AATAGAATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ACGGAGATGT TGAAGAAGCT 1920 GTTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAAGCCAGG AATGGTAATT 2100
GGGATACATAG TACTTAGAGG CGATGGTTCA ATTAGCAATA GGGCAAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTTCCA 2220 GCGGTACTTA GGGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATAACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

53/186

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-(HMf-like) fusion protein (Fig. 17-H)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATGAAGA GTTAAGAAGA GTTAAGCATG AAGCCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG XXXGAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAAGT 420 TCTTGCCTTC CGGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAAATGATT 480 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAAATA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGAATAT GACGGCTGTA GAAGTCAAGG GAAGAAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCCTATAT CCCTCGATTA TAAITACCCA
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGAGT TAGTATGGAA GGAGCTCGAA 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGAGGT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAAGCCAGG AATGGTAATT 2100
GGGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
2328

//ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA CAC CTT GAG GAA    108
AAA GCT ATT GAG GCA AAA AAG GCA GTA GAT CTT GCA GAT CTT GCA CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

## (HMf-like)-PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein (Fig. 17-1)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA CAC CTT GAG GAA    108
AAA GCT ATT GAG GCA AAA AAG GCA GTA GAT CTT GCA GAT CTT GCA CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATTGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAG AGTTTCTCGG CAAGCCTATT 240 ACCGTGTTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAGGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG GAAGTCAAGG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAAACT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTTCT ACTTAGGGAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAGC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGGT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGCAA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC TGGGAAGCGAT AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG

1680 GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGGAGA GGTATGCAGT AATAGATGAA TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGACG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGGATTGGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG
2328

## (HMF-LIKE)-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

### (Fig. 17-J)

D141A/E143A Mutant (GGN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC CTT ATA AGA AAG GCT GGT    54
   GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC TTT GAA     108
   AAA GCT ATT GAG GTC ATC GCA GTA AAG GCA GTA CTT GCA GAT CTT GCA AAG GAG GAA   162
   AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGACTGAAA GATTGAAGAA GTTAAGAAAA TAACGCATGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCAGCA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTGGTGA 660 AAAAGGGCAG TTTCGACTTG 780 TATCATGTAA TACGCCGACG AGATAGCAAA 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG TTCTGACTTG 780 TATCATGTAA TACGCCGACG AGATAGCAAA AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGGCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTTCT ACTTAGGAAA
1080 GCCTACGAAG GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA
GCTACACAGG .TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAAGTTTTCT AAATCTTGA GGGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320

AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT GCAAATTCTT TCTACGGATA TTATGGCTAT
1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAGAAAAG 1560 TACATCGAGT TAGTATGGAA
GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGGATT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATACC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA
TTACATGAGT ATAAGGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTGAAA TAAAGCCAGG AATGTTAATT
2100 GGATACATAG TACTTAGGAG CGATGGTCCA ATTAGCAATA GGGCCAATTCT AGCTGGAGAA 2160 TACGGATCCCA AAAAGCACAA
GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA TACAGAAAAG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //

2328

TGA

## PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein
### (Fig. 17-K)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAG TTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTGTTAG TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG GAAGTCAAGG GATTAAATTA ACCATTGGAA GATTAGGGAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATGGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGACGA AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGGAT TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA
GCTACACAGG .TGGATTCGTT AAAGAGCGAAG AGCTCCAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT AAAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320

57|186

AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGAGGAA
ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAGCGGAT AAACTCTTTA GCAAATTCTT TCTACGGATA TTATGGCTAT
1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGGACG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT GGAGGAGAAA GTGAGGAAAT
GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT AATAGAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT TTTGGAGACA ATACTAAAAC ACCAGAGAAG 1980 CTCGCAATAT AACAAGACCA
TTACATGAGT ATACAGGCGAT AGGTCCTGAC ATGAAATCC ACCAGAGAAG GGCAATTCT AGCTGCTAAA GGAGTTAAAA GGCCAGGAAATGGTTAATT
2100 GGATACATAG TACTTAGGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGCTAAA GGAGTTAAAA GGCCAGGAAATGGTTAATT
GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA ATTAGCAATA GGGCAATTCT GGAATATTGGA TACAGAAGG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
                                                                                      2328

//ATG GGA GGA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA  162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA AAG CTC AAG AGC TGA

## KOD DNA POLYMERASE - (HMf-like) fusion protein (Fig. 17-L)

**V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)**
**V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)**

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCAAGATA 300
CGGAGGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGGAAG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCGGTC GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAAACTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840

GCCGTGCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGGATGGA GCCCAGCTTT CTCGCGTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTGGACGTT 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGGAAGGAG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCGCCACGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGGAGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGGCT TCTTGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGAGCGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG AGGTCGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAGAAAGCTG AGCAAGTACG GTGACGTCGA GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC      CTT ATA AGA AAG GCT GGT 54
   GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
   AAA GCT ATT GAG ATC GCA AAG AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
   AAG ACC GTT AAG GTC GAA ATT AAG CTC GCA ATT AAG AGC TGA

(HMf-like) - KOD DNA POLYMERASE fusion protein (Fig. 17-M)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

```
GCT CAG AGA GTT AGC GAG CAA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108
AAA GCT ATT GAG ATC GCA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG  60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC  120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA GAGGCACGGG              180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXXC CAGCGATAAG GGACAAGATA  300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGCGGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA  660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGTTGCCGC CGAGCCGAAG  720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAAACTG CCCACATACA CGCTTGAGGC CGTTTATGAA  840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAAATAACCAC AGCCTGGGGAA 900
ACGGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGGATGG AAGATGCCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA  1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA  1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCACACAA CGTCTCGCCG  1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC  1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG  1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGGAGGAA GCTCCTCGAT  1440
TACAGGCAGA GGGCCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA  1500
AGGGCGCGCT GGTACTGCAA GGAGAGCGTAA CGGCCTGGGG AAGGGAGTAC AAGGGAGTTT  1560
ATAACGATGA CCATCAAGGA GGAGTGTGCA AAGTACGGCT TTAAGGTAAT CTACAGCGAC  1620
ACCGACGGAT TTTTGCCAC AATAACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT  1680
ATGGAGTTCC TCAAGTATAT CTTCGTCACG CGCTTGAGCT CGAGTACGAG ATGCGAGGAA  1740
GGCTTCTACA TCAAGTATAT CTTCGTCACG AAGAAGAAGT CGGGGTTGAT AGACGAGGAA  1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA  1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG  1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG  1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT  2040
```

GCGGGTTGCCA AGAGGTTGGC CGCGGAGGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

(HMf-like)-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-N)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
   GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
   AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
   AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT   120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA   180
AAAACTGTGA GAGTGGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT   240
GAAGTCTGGA AGCTCATTTT CGAGACATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA   300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT   360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT   420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTGGAA AGGGCGAGAT AATAATGATT   480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT   540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAAGCGTT TTGTTCAAGT TGTTAAAGAA   600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA   660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA   720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT   780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT   840
TATGAAGCAG TTTTAGGAAA AACCAAAGC CAGAGGAAAT TGCCGCTATA   900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA   960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGGAGGAA TGAACTTGCA CCGAATGAGGA AGAGTATAAA AGGTTTGTGG 1140
CGGCGCTTAA GAACAACTTA CCTGGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200

61/186.

GAAAATATCA TTTATTTGGA TTTCCGCGAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGCAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTGA AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCAATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGGAGC GGAAAGATAA GCGATAGGGT AATTTACTT. 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGAATGCA TGGCTCAAGA GGTAG 2325

Vent DNA POLYMERASE - (HMf-like) FUSION PROTEIN (Fig.17-O)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACAATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCGATCCC CAGCTATGCG CAAGAC<u>XXXC</u> 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGAGGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGGATGTTG TGTTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660

AAACGGGGCAG AAAAGCTGGG AGTTCGGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGAGTTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GGAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTGTA AGAGTTGTTA GAGAGAAGAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGAATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

Deep Vent- (HMf-like) DNA polymerase fusion protein (Fig. 17-P)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAG AAG GCA GTA GAT CTT GCA GAT CTT GCA GGT GAG GAA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```
V93R MUTANT:  XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT:  XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG     60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT    120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGGAAG ATAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTTAAGGAAGA AGTTCCTGGG GAGGCCGATT   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT    420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC    540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT    660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG    720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC    780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG    840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC    960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC   1020
CTGTGGGATG TTTCTAGGTC TTCAAACTGG CAACTTGGTG GAGTTGTACCT CCTCAGGAAG  1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAAG   1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG   1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA   1260
CCGGATACGC TGAACAGGGA AGGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC  1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC TCTAAAGACC TCAAGGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAGAAGAA GAAGATGCTT ATTATGGGTA  1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAGACGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA   1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC   1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG   1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATCCTAAGGC GGGACTGGAG CGAAAATAGCC  1860
AAAGAAACCC AAGCAAAAAG CCTAGAGGCT ATCCTAAAGC CGGAGGAGGCA CGAAATAGCC  1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAGAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACGAAGGCTAT AGGTCCGCAC  2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGGGTTAAAG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
```

```
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTTACCT  2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGGTCTTAC AACATCAAGA AGAAG //                           2328
```

```
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
  GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
  AAA GCT ATT GAG ATC GCA GAG AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
  AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

(HMflike) - Deep Vent DNA polymerase fusion protein (Fig. 17-Q)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
  GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
  AAA GCT ATT GAG ATC GCA GAG AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
  AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

```
//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG   60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTTAAGGAAGA AGTTCCTGGG GAGGCCGATT  240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCCAATAAG GGATAAGATA  300
AGAGAGCATT CCGGAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGGATGAAG AGCTCAAGTT GCTCGCATTT  420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAACGTGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGGATACA  CTTTGACCTC              780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA AGATAGCTGA AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC  960
```

es/186_

GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGGAAAG 1140
CTAAGGGAGA GCTACGGCTG GGGATACGTT AAGGAGCCCG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGACG TTACGACGTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTAGTTGGTT GATAGATGAG 1800
GAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGACAGAT CACGGAGGCC CTTCAGGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAG TGAGGCCTGG CATGGTGATA 2100
GGGTACAATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GAATATTAGA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGGAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

JDF-3 - (HMf-like) fusion protein (Fig. 17-R)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCATCAGGGTCTTCAAGGAGAACGGCGAGTGGAATACGACCGAGTTCGAGCCCTACTTCT
ACGCGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAACGGGGAGGGCACGGCGGTCGTTAAGGTTAAGCGCGGGAGGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCTTGTGGAGGTCTGGGTCTCCTTACTTCACGCACCCGACAAAATAAGGAAGCACACCCGGGGTCAATCCGGACAAAAATAAGGAAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGCCTTAATCCTGATGGAAGAGCTTAAACTGATTCATGTCCTTCGACATCGAGACGCTCTCACCACGAGGGGGAGAGGAGAAGAA
CCGGGCCGGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCACTTCGGGAGTTGTGTTCTCCACCGAGAAGCTTGAGAAGGGCGTGAGCTTT
GGCTTCTTGAGGGTCGTTAAGGAAGACCGAGCACGGTGGCTGATAACATACAACTTCGACCTTCGAAAAAGCGCTTGTTGAGAAGCTTGGGCGTGAGCTTA
ACCCTCGGGAGGGGACGGGAGCGGAAGAATACAGCGCAATGGGGACAGTTTGCGGGTCGAGGTGAAGGGCGTACACTTCGACCTTTATCCAGTCATAAAGGGCGCACCATAA

ACCTCCCGACCTACACCCTTGAGCTTGGCTGTATACGGGGTTTTCGGCAAGGAGGAAGGTCTACGCCGGAGAATAGCCACCGCCCTGGGGAGGACCGGGAGGGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGGGTTACTACGAGGAGTTCTTCCCGATGGGAGGTCTCATCGGCCAAGGCCTTCATCGGCCAAGGCCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTTGGCAGGGAGTTCTTCCCGATGGGAGCTTTCCAGGTGAGGCTCATCGGCCAAGGCCGACGTTTCC
ACgcCGGTGGCTACGTCAAGGAGGCCGGAGCGGGGGACTGTGGGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTTCTACGCCTTCAATCATAATCACCCACAAACGTCTCGCCGAGATAC
GCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGACTTCCCGCTTCATTCGGAAACCTGCTCGGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGGAAGAAGAATCTCCTGATTACAGGCAAGACGCGCCATCAAGAATTCTCGCCAACACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGAAGTGGTACTGCAGGGAGTGCGCCGGAGGCGGTTACGGCCATGGGAAGGGGAGTACATCGAAAATGGTCATCAGAGAAAAGTTCGGGTTTTAAAGTCCT
CTATGCAGACACAGACGGGTCTCCACCATTCCTGAAGGAAGGGGGGGGAGTTCTTAAACTATATCAATCCCGGGCCTTCTC
GAACTCGAATACGAGAGGGCTTCTCTTCGTCACGGACGAAGAAAGTACGCCGGTCATCGAAGAAATTGTCAGGAGAATAACCACGCCTTGAAGAAAAGCTGAGCAA
ACTGGAGCGAGATAGCGAAGGAGGACGCGAGGGTTTGGGAGACGGTTTATCCACGGAGATAACGCGTCAAGGACGTTGAAGAGGCGGTTCAGGAAGTTCACGAAAAGCTGAGCAA
GTACGAGGTTCGCGCGGAGAAGCTGGTTTATCCACGGAGATAACGCGTCAAGGACTACAAGGCCACCGGTCGCATAGCCAGGAAAGCTTGAGCAA
GTTAAAATCCGGCCCGGAACTGTGATAAGCTACACATCGTTCTGAAGGGCTCCGGAAGGGATAGGCGCTACAAGGCCACCGGTTCGCAATAGCCAGGAAAGCGTTTGGCGCCAGAGGT
CGGACTACTACATCGAGAAACCAGGTTCTGCCCGGACGTTGAGAGAATCCTCAGGCCTTCGGCTACCGCGCAAGGAAGAGACCTGCGCTACCAGAAGACGAGGTCGGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

(HMf-like) - JDF-3 fusion protein (Fig. 17-S)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCGTCATCAGGGTCTTCAAGGAAGAGAACGGCGAGTTCAGGATTGAATACGGACCGCGAGTTCGAG
CCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACGCGGGAGGCCAGGGTCGTTAAGGTTAAGCGCGCGGGAAGGT
GAAGAAAAGTTCCTCGGCAGTCTGTGGGTCCTCCTACTTCACGCCACTGTTTCGCTGAGGTCTTCGGGAGGTGAGGAGAAGGGGGGGCT
TCGACATCTCAGAGTACGACACATACCCTTCGTGGGGAGGTCTCAAGCGCGTACCTCAGGAAGTTGAGGAGAGGCTTAAACTCATGTCCTTCGATC
GAGACGCTCTACCAGGAGGAGAGTTTGGAACCGGGCCGATTCTGATGACAAGCGGCGGCCTAACTCCGATGAGTGAAGTTGAGGAGAGCTTAAACTCATGTCCTTCGGAC
TCCTTACGTTGAGGTTGTGTCTCCACGGAGGAAGGAGAGAGTATTAAGCGCGCTTCCACGGGGTCGTTAAGGGTTCGTTAAGGAAGAGAGATCGGACT

TCGACTTCGCCTACCTGAAAAAGCGCTGTGTGAGGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGACGGGGAGCGAGCCGGAAGATACAGCGCCATGGGGGGACAGGTTTGCG
GTCGAGGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCCACCATAAACCTCCGACCCTTGAGCGTGTATACGAGGCGGTTTTCGGCAA
GCCCAAGGAGGAAGGTTCACGGCCGAGGAGATAGCCACCGCCTGGGAGACCGGGCTTGAGAGGGTCGCGGCCTACTCGATGGGAGGACGCGAGGGGTTACCTACG
AGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGTACGTTTCCCGCTCCAGCACGGCAACCTCGTCGAGTGGTTC
CTCCTAAGGAAGGCCTACGAGGAACGAACTCGCTCCCAACAAAGCCCTGGCGAGGAGGCTACgccCGGTGGGCTACGTCAAGGAGCC
GGAGCGGGGACTGTGGGACAATATCGTTGTATCTAGACTTTCGTAGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGT
GTAGGAGCTACGACGTTGCCCCGGAGGTCGGGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGGAAACCTGCTGGAAAGGCAGAAGATA
AAGAGGAAGATGAAGGCAAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGCGATCAAGAGAATTCTCGCCAACAGCTACTACGGGCTA
TGCCAGGGCAAGAATGGGTACTGCGCCGAGAGCGTTACGGGCCATGGGGAAGGAGTACAGGCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTA
AAGTCCTCTATGCAGACACAGAGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAAACAGTCAAGAAGCAATGGAGTTCTTAAACTATATCAATCCCAA
CTGCCCGGGCCTTCTCGAATACGGAGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGCGCGCGACTGGAGCAGGCGAGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAA
TTGTCAGGGAAGTCACCGAAAAGCTGAGCGAGGTTCCGCCGGAAGCTGGTTATCCACGAGCTCAAGGACTACAAGGCCACCGGC
CCGCACGTAGCCATAGCGAAGcGTTTGGCCCGACGAGGTGTTAAATCCGGAGGAACTGGATAAGCTACATCGTTCTGAAGGGCTCCGGAATAGGCGACAG
GGCGGATTCCTTCGACcGAGTTCGACCCGGACTACTACATCGAGAACCAGGTTCTGCGGCAGTTGAGAGAATCCTCAGGGCCTTCG
GCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGCTTGGGCGTGGGCTGA

ACCESSION No: AE010210 REGION: complement (8333..9082) (Fig. 17-T)
/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

```
M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC        18
                                                                                54

T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA        36
                                                                               108

S   M   R   A   M   D   P   S   R   V   L   I   D   L   N   L   P
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT CTG ATT GAC CTA AAT CTC CCG            54
                                                                               162

S   S   I   F   S   K   Y   E   V   V   E   P   T   I   G   V   N
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTC CCA GAA ACA ATT GGA GTT AAC            72
                                                                               216

M   D   H   L   K   K   I   L   K   R   G   K   D   T   L   I
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GAC ACC TTA ATA                90
                                                                               270

L   K   G   E   E   N   F   L   E   I   T   I   Q   G   T   A   T
CTC AAG GGA GAG GAG AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA           108
                                                                               324

R   T   F   R   V   P   L   I   D   V   E   E   M   E   V   D   L   P
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA       126
                                                                               378

E   L   P   F   T   A   K   V   V   V   L   G   E   V   L   K   D   A
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTT CTA AAA GAT GCT       144
                                                                               432

V   K   D   A   S   L   V   S   D   S   I   K   F   I   A   R   E   N
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA GTT TTT ATT GCC AGG GAA AAT       162
                                                                               486

E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T
GAA TTT ATA ATG AAG GCA GAA GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT           180
                                                                               540

L   E   D   E   G   L   L   D   I   E   V   Q   E   E   T   K   S   A
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA       198
                                                                               594

Y   G   V   S   Y   L   S   D   M   V   K   G   L   G   K   A   D   E
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA       216
```

69/186

```
                                                                              Y   G   V   S   Y   L   S   D   M   V   K   G   L   G   K   A   D   E
                                                                              TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA    648

V   T   I   K   F   G   N   E   M   P   M   Q   M   E   Y   Y   I   R
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA    234  702

D   E   G   R   L   T   F   L   L   A   P   R   V   E   E   *
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA    250  750
```

(PCNA)-Taq DNA polymerase fusion protein (Fig. 17-U)

```
M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    18   54

T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAT GGG ATA    36  108

S   M   R   A   M   D   P   S   R   V   V   L   I   D   L   N   L   P
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG    54  162

S   S   I   F   S   K   Y   E   V   E   P   E   T   I   G   V   N
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC    72  216

M   D   H   L   K   K   I   L   K   R   G   K   A   K   D   T   L   I
ATG GAC CAC CTA AAG AAG ATC AAA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA    90  270

L   K   G   E   E   N   F   L   E   I   T   Q   G   T   A   T
CTC AAG GGA GAG GAG AAC TTC TTA GAG ATA ACA GGA ACT GCA ACA    108  324

R   T   F   R   V   P   L   I   D   V   E   E   M   E   V   L   K   D
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT CTA AAA GAC    126  378

E   L   P   F   T   A   K   V   V   L   G   E   V   L   K   D   A
GAA CTT CCA TTC ACT GCA AAG GTT GTA CTT GGA GAA GTC CTA AAA GAT GCT    144  432

V   K   D   A   S   L   V   S   D   S   I   K   F   I   A   R   E   N
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT    162  486
```

```
E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T        180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT     540

L   E   D   E   G   L   L   D   I   E   V   Q   E   E   T   K   S   A        198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA     594

Y   G   V   S   Y   L   S   D   M   V   K   G   L   G   K   A   D   E        216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA     648

V   T   I   K   F   G   N   E   M   P   M   Q   M   E   Y   Y   I   R        234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA     702

D   E   G   R   L   T   F   L   L   A   P   R   V   E   E                    250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG

G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
```

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L S D R I H V L H P E G Y
GAC CTT TAC CAG CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGC TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCG GAC CGG GAG AGG CTT

R A F L E R L E F G S L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA CCC AAG GCC CTG GAG GAG GCC CCG TGG CCC CCG GAG GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTG CTG GCC

L A A R G R V H R A P E P Y K A
CTG GCC GCC AGG GGG CGG GTC CAC CGG GCC CCT TAT AAA GCC

Fig 17U (cont)

72/186

```
L   R   D   L   K   E   A   R   G   L   A   K   D   L   S   V   L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A   L   R   E   G   L   G   L   P   P   G   D   D   P   M   L   L   A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCG ATG CTC CTC GCC

Y   L   L   D   P   S   N   T   T   P   E   G   V   A   R   R   Y   G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCG GAG GGC GTG GCC CGG CGC TAC GGC

G   E   W   T   E   E   A   G   E   R   A   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCA GCC CTT TCC GAG AGG CTC TTC

A   N   L   W   G   R   L   E   E   G   E   R   A   L   L   W   L   R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG CGG GCC CAC CTT TGG CTT TAC CGG

E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
CGC CTG GAC GTC GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A   R   L   E   A   E   V   F   R   L   A   G   H   P   F   N   L   N
GCC CGC CTC GAG GCC GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S   R   D   Q   L   E   R   V   L   F   D   E   L   P   A   I
TCC CGG GAC CAG GAA AGG GTC CTC TTT GAC GAG CTA CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC AGC ACC AGC GCC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   A   T   G   R   L   S
GGC CGC CTG CAC ACG CGC TTC AAC CAG ACT GCC ACT GCT ACG GGG CGG CTC AGC
```

Fig 17 U (Cont)

```
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

 S   S   D   P   N   L   Q   N   I   P   V   R   T   P   L   G   Q   R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I   R   R   A   F   I   A   E   E   G   W   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S   Q   I   E   L   R   V   L   A   H   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC TCC GGC GAC GAG AAC CTG ATC

 R   V   F   Q   E   A   V   D   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GCC GTG GAC CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC GCC AAG ACC ATC

 N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

 V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K   S   V   R   E   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GAG CGC ATG GCG TTC AAC ATG CCC GTC CAG GGC

 T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

 E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTC GTC CTC GAG GCC
```

```
P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT

H   H   *
CAT CAT TAA
```

Taq DNA polymerase- (PCNA) fusion protein (Fig. 17-V)

```
            G   G   G
         // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTC TTC GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCC GGG CGG GCC CCC

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG
```

```
L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC GGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG TGG GGG AGC CTG GAA

A   L   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCG GAC CGG GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   S   L   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   A   P   W   P   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCG CCC CCG GAA GGG GCC

F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
CTG GCA GCC CGC GGG GGC CGG GTG CAC CGC GCC CCG GAG CCG TAC AAG GCC
```

```
        L   R   D   L   K   E   A   R   G   L   L   A   K   D   L   S   V   L
CTG GCC GCC GCC AGG GGG GGC GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
    CTC AGG GAC CTG AAG GAG GCA CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

        A   L   R   E   G   L   L   P   P   G   D   D   P   M   L   L   A
GCC CTG AGG GAA GGC CTG CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

        Y   L   L   D   P   S   N   T   T   P   E   G   V   A   R   R   Y   G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCG GAG GGG GTG GCC CGG CGC TAC GGC

        G   E   W   T   E   E   A   G   E   E   R   A   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG GGG GAG GAG CGG GCC GCC CTT TCC GAG AGG CTC TTC

        A   N   L   W   G   R   L   E   G   E   E   R   L   L   W   L   Y   R
GCC AAC CTG TGG GGG AGG CTG GAG GAG GAG CGG CTC CTT TGG CTT TAC CGG

        E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

        R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAC CAC GTG GCC GAG ATC

        A   R   L   E   A   E   V   F   D   E   L   G   H   P   F   N   L   N
GCC CGC CTC GAG GCC GAG GTC TTC GAC GAG CTC GGC CAC CCC TTC AAC CTC AAC

        S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

        G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTT CCC GCC

        L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

        K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
```

```
G   R   L   H   T   R   F   N   Q   T   A   T   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S   S   D   P   N   L   Q   N   I   P   V   R   T   P   L   G   Q   R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I   R   R   A   F   I   A   E   E   G   W   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S   Q   I   E   L   R   V   L   A   H   L   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R   V   F   Q   E   G   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG CGG GCG GCC AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCG GAG CGC ATG GCG AAC ATG CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
```

```
P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GGC ATA GGG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT

H   H   //  //
CAT CAT  //

M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D          18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54

T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I          36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT GAC GAA GAT GGG ATA      108

S   M   R   A   M   D   P   S   R   V   V   L   I   D   L   N   L   P          54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162

S   S   I   F   S   K   Y   E   V   E   P   E   T   I   G   V   N             72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC          216

M   D   H   L   K   K   I   L   K   R   G   K   A   K   D   T   L   I          90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270

L   K   G   E   E   N   F   L   E   I   T   Q   G   T   A   T                 108
CTC AAG GGA GAG GAA AAC TTC TTA GAG ATA ACA CAA GGA ACT GCA ACA             324

R   T   F   R   V   P   L   I   D   V   E   E   M   E   V   D   L   P          126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378

E   L   P   F   T   A   K   V   V   V   L   G   E   V   L   K   D   A          144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
```

Pfu DNA Polymerase (WT)-(PCNA) fusion protein (Fig. 17-W)

```
V   K   D   A   S   L   V   S   D   S   I   K   F   I   A   R   E   N      162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   486

E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T      180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540

L   E   D   G   L   D   I   E   V   Q   E   E   T   K   S   A             198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA   594

Y   G   V   S   Y   L   S   D   M   V   K   G   L   G   K   A   D   E      216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648

V   T   I   K   F   G   N   E   M   P   M   Q   M   E   Y   Y   I   R      234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA   702

D   E   G   R   L   T   F   L   A   P   R   V   E   E   *                 250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA
```

```
cctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatataa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtgaga aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
```

//

```
tttggaacat cccaagatg  ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gaggggaaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gattctcag  gattatcaag gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
cctccaatg  gaaattcag  tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagctacg  aaagaaacga
agtagctcca aacaagcaa  gttgaagaga gtatcaagg  aggctcaagg agagctacac
aggtggattc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgaggggatgc aagaactatg atatcgctcc tcaagtagc  cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
```

```
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaaggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggccgatggt ccaattagca ataggccaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggatt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttttattctt
tctaaccttt ttctatgaaa gaagaactga ccaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcctgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
```

```
ctatctgcat gcttctctgg ctcggaaatg gaggattcat aacaacagta tcaacattct
cagagaattg agaaaacatca gaaactttga cttcctacaac atttctaact ttgcaactct
tcaagatttt ctaaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct
ttccggggat tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taactttac agaaataact gtctcaaatt atgacaactc ttgacaatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagacttta
gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttccttgg //
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC     54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT ACA GAA GAT GGG ATA            108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT AGA GTT GTC ATT GAC CTA AAT CTC CCG  162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC        216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA GAA GAC TTA ATA        270
CTC AAG AAA GGA GAA AAG TTC TTA GAG ATA ACA ATT CAA AAG ACC GCA ACA        324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GGA ACT GCA CCA  378
GAA CTT CCA TTC ACT GCA AAG CTA GTT CTT GGA GAG GTC CTA AAA GAT GCT        432
GTT AAA GAT GCC TCT CTA GTG AGT GTT AGC ATA AAA TTT ATT GCC AGG GAA AAT    486
GAA TTT ATA ATG AAG GCA GGA GAA ACC CAG GAA GTT GAG ATA AAG AGG CTA ACT    540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA        594
```

TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT AAG GCC GAT GAA   648
GTT ACA AAG TTT GGA AAT CCC ATG CAA ATG GGA TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-X)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAA GAT GGG ATA    108
AGC ATG AGG GCC ATG ATA CCA AGT AGA GCC CTG ATT GAA AAT CTC CCG    162
TCA AGC ATA TTT AGC AAA TAT CAA GTT GTC ATT CTA AAC ACA ATT AAC    216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GCA GAA GAC ACC TTA ATA    270
CTC AAG AAA GGA GAA AAG TTC TTA TTA AAG ATT CAA AAG GAC ACA    324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG ATG GTT GAC CTC CCA    378
GAA CTT CCA ACT GCA AAG GTA AAG GTT CTT GAA GAG ATT GAC CTC AAA GAT GCT    432
GTT AAA GAT GCC TCT CTA GTG AGT TAT CCA ATA GAA ACA TTT GAT ATT GCC AGG GAA AAT    486
GAA TTT ATA ATG GCA GGA GAA ATC AAC GAA GTT CAG GAA GTT GAG ACA ATA ACT    540
CTT GAA GAT GAG TTA CTT GAC GAT GGA GTT CAG GAA ATA AAG AGC GCA    594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT AAG GCC GAT GAA    648
GTT ACA AAG TTT GGA AAT CCC ATG CAA ATG GGA TAT TAC ATT AGA    702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG
```

//

```
ccctggtcct gggtccacat atatgtctt actcgcctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatatagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgatt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttagaac atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
```

Fig 17.X (con't)

```
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaactta
tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctta
tcacgaagga gaagagtttg gaaaaggccc aattatatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcaag gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
cccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggttggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatccgctcc tcaagtaggc cacaagttct gcaaggacat
```

Fg 17X (cont)

```
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atccatataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtccctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaggt tttataagag
gggattcttc gttaegaaga agaggtatgc agtaatagat gaagaagaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaaagaaa ctcaagctag
agtttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtaggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaaataaagc aggaaatggta tagtacttag
aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggaggatttt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaacctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccccatg ctcttgggag aatcttcgaa taaaatccct aacttcaagc
```

87|186

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccggggagt tttgtattgc tctagccaag gttggggatt tttgaatcct ttaactctgg

aaagtatat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taactttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gttttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactccaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg // TGA

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein (Fig. 17-Y)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108

AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA AGT CCA GAA GAC ATT AAC   270
CTC AAG AAA GGA GAG AAC ATC CTA ATA GAT TTC TTA AAG AGA GCA ATT CAA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GTA GAG ATA ACA ATT CAA GGA   378
GAA CTT CCA ACT GCA AAG GTT GTA CTT GAA GAG ATG GTT GAC CTC CCA   432
GTT AAA GAT GCC TCT CTA GTG AGT GTT GTT ATT GCC AGG GAA AAT GCT   486
GAA TTT ATA ATG GCA GGA GGA ACC AGC GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GGA TTA TTG GAC GTT CAA GAG GTT GAG ACA AAG AGC ACT   594
TAT GGA AGC TAT GGA ATC GAA AAA TTT GGA CTT GAG AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT CTC CTA CTG GCT CCA AGA GTT GAA GAG   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGAATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTGACTGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGGAA
TGGATTCGTT AAAGAGCCAG AAAAGGGGTT 1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGGCAAGTA GAGAGGAGTA
TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GTGGGAAAAC AACTATGATA TCGCTCCTCA AGTAGCCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTAATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGGAGGAGAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGGAG
TGAAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAAGCT 1920 GTGAGAAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG AGCTGCTAAA 1980 CTCGCAAATAT ATGAAGCAGAT AACAAGAACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA AATGGTAATT 2100

GGATACATAG TACTTAGAGG CGATGGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA
2328

<u>PFU DNA POLYMERASE (V93 R OR E)-(PCNA) fusion protein</u> (Fig. 17-Z)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTGA GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAAACT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGAGTTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTTGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTTAGCG 660 AAAAAGGGCAG GAAGTCAAGG AAGAATACTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG AAGAATACTA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG
TGGATTCGTT AAAGAGCCAG AAAAGGGGGT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCCGATACTC TAAAATCTTGA GGGGACATTT GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACCTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA AAAGAAAAAG
1680 GCTCCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA

GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
2328

ATG CCA TTT AAG ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54

ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGT AGA GTT GTC ATT GAC CTA AAT CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT AGA GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG AAG AAC TTC TTA GAG ATA ATT CAA GGA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GAG GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GAA GAG ATG GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT AGC ATA AAA TTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GCA GGA GGA GAA ACC CAG ATA AAG AAA CTA ACT   540
CTT GAA GAT GAG GGA TTA GAG GTT CAA GAA GTT GAG ACA ATA AGG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC TTG GAC GTT AAA GGA GAG TAT TAC ATT   648
GTT ACA ATA AAG TTT GGA AAT CCC ATG CTT GGA GAG AAG GCC GAT GAA   702
DAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein(Fig. 17-AA)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTGAAGAA GTTAAGAAAA TAACGGGGGA AGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTGAGAGAA GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACCATTC TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAACGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCAATTGGAA CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAGAGTTAT GGAGAAGGTA TACGCCGACG AATAGCAAGG CGAGCCCAAG 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT ACCTTGTGCCAA TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA

1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCCTACACTT 1620 GACACTGAGA GTCTCTATGC AACTATCCCA GGAGGAGAAA AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAGCTCA AAGCTCCCTG GACTGCTAGA GCTTGAAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGGAGA GGTATGCCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAGGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980 CTCGCAAATAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACAATA TACTTAGGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT ATA GTC ATT GAA AAT CTC CCG   162
TCA ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA GAA GTT AGA GGA GAC ACC TTA ATA   270
CTC AAG AAA GGA GAA AAC TTC TTA AAG ATT CAA AAG GGA ACT ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AGT GTT CTT GAA GTC CTA AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT GTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GCA GGA ACC CAG GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GGA TTA TTG GAC ATG GAG CTT GGA ACA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC GTT AAA GGA GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GAA CAA GTT GAG AAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA)- PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein (Fig. 17-BB)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT ACA GAA GAT GGG ATA          108
AGC ATG AGG GCC ATG ATA CCA AGT AGA GTT GTC CTG AAA GTT CTC CCG          162
TCA AGC ATA TTT AGC AAA TAT GAA AGT AGA GTT GAA CCA ACA ATT AAC          216
ATG GAC CAC CTA AAG AGA ATC CTA AAG AGA GGT GAA GTT GGA GTT ATA          270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA CAA AAG GCA ACA          324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG ATA GAC CTC CCA             378
GAA CTT CCA ACT GCA AAG GTT CTT GAA GTC GAA AAA GAT GCT                 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA GCC GAA AAT                 486
GAA TTT ATA AAG GCA GGA ACC CAG ATA AAA TTT GCC AGG CTA ACT             540
CTT GAA GAT GGA TTA CTC GAG GGA GTT CAA GAA GTT GAG GAG CTA ACT         594
TAT GGA GTC AGC TAT GGA ATG AAA GGA CTT GAG GAG ACA AAG AGC GCA         648
GTT ACA ATA AAG TTT GGA AAT CCC ATG AAA GTT GAG GAG TAT TAC ATT AGA     702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
```

```
//ATGATTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGAATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC AGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG GAAGTCAAGG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGCA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCGATACTTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACACATT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
```

CTATAGAAA AATACTCCTT 1440 GACTATAGAC AAAAAGGCGAT AAAACTCCTTA GCAAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTAAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAATG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAATAT ATGAGGGATAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AAATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGCGTTG ATTAGCAATA GGGCAAATTCT AGCTGCTAAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG

2328

(PCNA)-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein(Fig. 17-CC)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA ATA TTT AGC AAA TAT GAA GTT GTT GTA AGT TTG GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT GAA GAC ACC TTA ATA 270
CTC AAG AAA GGA GAA AAC TTC TTA AAG ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA CCC CTA ATA GAT GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GAA GAG ATA AAA GAT GCT 432
GTT AAA GAT GCC TCT GTG AGT GAC AGC ATA AAA TTT ATT GCC GAA AAT 486
GAA TTT ATA ATG GCA GAG GGA ACC CAG GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GGA TTA TTG GAC GTT CAA CTT GGA GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA CAA ATG GAG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA CAA GTT GAA GAG //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTGAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180

TGA

```
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAAATGATT 480 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTGGTTA TACTTCATAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGAGCCCAA CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGGGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAAATGGA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA
GCTACACAGG.TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT 1260 CCGGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT GTTAGAGCGG GCAAATTCTT TCTACGGATA TTATGGCTAT
1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA
GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAGAT CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCGAGT AATAGAGTAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAACAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA
TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT
2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA
GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGGTACTTA GGATATTGGA GGGGATTTGGA TACAGAAAAG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
                                                          2328
```

<u>PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein (Fig. 17-DD)</u>

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG AATGTGGATGA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAAGTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATGAAGAA GATTGAAGAA GTTAAGAAAA AAGGCATGGA 180
```

fig. 17 DD (cont)

```
AAGAATTGTTGA GAATTGTTGAG TGTAGAGAAAA AGTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAAATGATT 480 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTTGGAT TACTTATAGT
GGAGACTCAT TCGGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGGATG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGGAGA
GCTACACAGG.TGGATTCGTT AAAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAGCGGAT TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TTATGGCTAT
1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TTATGGCTAT
GGAGCTCGAA GAAAAGTTTG GATTGTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGGAGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCAATTACTCG TGGTTTAGGA ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGAGTGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAATAT ATGAGCGAGAT AACAAGACCA
TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AAATGGTAATT
2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA
GTATGACGGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATAATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
```

```
// ATG CCA TTT GAA ATC GTA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC          54
   ACC GCA AGT AAG TTA GAT GAG GCC GCG TTT ACA GAA GAT GGG ATA             108
   AGC ATG AGG GCC ATG CCA AGT GTC CTG ATT GAC CTA AAT CTC CCG             162
   TCA AGC ATA TTT AGC ATG GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC         216
   ATG GAC CAC CTA AAG AGA ATC CTA AAG GGT AAA GAC ACC TTA ATA             270
   CTC AAG AAA GGA GAA AAC TTC TTA GAG ATT CAA GGA ACT GCA ACA             324
   AGA ACA TTT AGA GTT CCC CTA ATA GAT GGA ATG GAA GTT GAC CTC CCA         378
   GAA CTT CCA ACT GCA GTT CTT GGA GAG GTC CTA AAA GAT GCT             432
   GTT AAA GAT GCC TCT CTA GTG AGT GGA ATA TTT GCC AGG GAA AAT             486
   GAA TTT ATA ATG AAG GCA GGA GAA GTT CAG GAA ATA AAG CTA ACT             540
   CTT GAA GAT GGA TTA TTG GAC ATC GTT CAA GAA ACA AAG AGC GCA             594
   TAT GGA GTC AGC TAT CTC GAC ATG GTT AAA GCC GCC GAT GAA             648
```

```
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA    702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA
```

KOD DNA POLYMERASE - (PCNA) fusion protein (Fig. 17-EE)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC  120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG  180
ACGGTTGTAA CGGTTGAAAG GGTTGAGAAA GTTCAGAAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGGACAAGA GGACAAGATA  300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGGCGTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGCGGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTGAAGGAG  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG  600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA  660
AAGCGCTGTG AATAAACTTC CCCACATACA GGGATGAAGG CGAGCCGAAG CGAGCCGAAG  720
TATCCTGTGA TAAGACGGAC GATAAACTGG CCCACATACA GGGATGGAAG AGCCTGGGAA  780
ATTCAGAGGA GTTTGCCGTC CCCACATACA GGGATGAAGG CGGTTTATGA CGTTTATGAA  840
GCCGTCTTCG GTCAGCCGAA GATAAAGGCT TCGACTTCGC CTATCTGAAG GCCTGGGGAA  900
ACCGGCGAGA GGAGAAGGTT TACTCGATGG AAGATGCGAA AGGTCACATA GGTCACATAC  960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAGGAGGCT GGCCAGAAGA 1140
CGGCAGAGCT CTAGTGTAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA GGAGAACATA 1200
GTGTACCTCA ATGTACGTTG CCTAATCATCA TCAATCATCA CGTCTCGCCG CGTCTCGCCG 1260
GATACGGCTA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CGGCCACCGC 1320
TTCTGCAAGG CCATGTACCC TCAAATCATCA GAGGGTTGTG CGGCCACCGC AGAGGAGAGG 1380
CAGAAGATAA ACTTCCCAGG ATTTATCCCG AGCCTGCTTG CCCCACAGGT GCTCCTCGAT 1440
TACAGGCAGA GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT CGGCTATGCA 1500
AGGGCGCGCT GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA AAGGGAGTAC 1560
ATAACGATGA GGTACTGCAA GAGTCGTGCA CGGCCTGGGG AAGGGAGTAC CTACAGCGAC 1620
ACCGACGGAT CCATCAAGGA GATAGAGGAA AGTACGGCTT TAAGGTAATC AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCCAA CTTCCGGGGCG CGCTTGAGCT CGAGTACGAG 1740
```

GGCTTCTACA AACGCGGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGGTGAT AGACGGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGAATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGGTTGCCA AGAGGGTTGGC CGCGGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGTGC CTTCGGTTAC CGCAAGGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

(PCNA) - KOD DNA POLYMERASE fusion protein (Fig. 17-FF)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG TTA GAT CCA AGT AGA GTC CTG ATT GAC AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GTT GAA GTT GTT GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG GAC ATC CTA AAG AGA GGT AAA GCA GAA GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG AAG AAC TTC CTA AAG GTT ACA AAT GCA GAA GAA CTT GCA ACA 324

AGA ACA TTT AGA GTT CCC CTA ATA TTC TTA GAG ATA ACA ATT CAA GGA CTC CCA 378
GAA CTT CCA ACT GCA AAG GTA GTT CTT GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT TCT CTA CTA GTG AGT GTA GAT ATA GCC AGG GAA AAT 486
GAA TTT ATG GCA GGA GGA TTA AAG GAG ACC AGC ATA AAG AGG CTA ACT 540
TAT GGA GTC AGC TAT TCC GAC ATG GTT CAA CTT GGA GAG AGC GCA 594
GTT ACA ATA AAG TTT GGA AAT GCC ATG CAA CTT GAG GCC GAT GAA 648
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA 702

Fig.17 FF (con't)

```
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA  378
GAA CTT CCA TTC ACT GCA AAG GTC CTA AAA GAT GCT                          432
GTT AAA GAT GCC TCT CTA GTG AGT GTT ATA CTT GAA GAA AAT                  486
GAA TTT ATA AAG GCA GAG GGA GAA ACC CAG ATA TTT GCC AGG GAA ACT          540
CTT GAA GAT GGA TTA GAC ATC GAG GTT CAA GAA GTT GAG AAG CTA ACT          594
TAT GGA GTC AGC TAT GGA CTC TCC GAC ATG AAA GGA CTT GAG AAG GCC GAT GAA  648
GTT ACA ATA AAG TTT GGA AAT GAC ATG CCC ATG GAG CAA ATG GAG TAT TAC ATT AGA  702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
```

```
//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACGGGACTT TTGAACCCTA CTTCTACGCC   120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG   180
ACGGTTGTAA CGGTTAAGCG GGTTGAGAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGGATAAG GGACAAGATA   300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC   360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC   420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA   480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC   540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG   600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA   660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG   720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGAGATACA CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA   840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA   900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC   960
GAGCTTGGGA AGGAGTTCCT TCCGGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA   1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA   1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG   1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC   1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG   1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT   1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA   1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC   1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC   1620
ACCGACGGAT TTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT    1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGAGTACGAG              1740
```

GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGGAT AGACGGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGACGGA GATAGCGGAAA 1860
GAGACGGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

(PCNA)-Vent DNA POLYMERASE FUSION PROTEIN (Fig.17-GG)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTC CTG ATT GAC CTA AAT CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT AGA GGT GAA CCA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG GTT TTA GAG AGA ACA ATT GCA TTA ATA   270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA CAA AAG GGA GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG ATG ATT GAC GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GAA GTC GAA GTT GAC AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT GTT ATT TTA GAG ATG ATC AAA GAA AAT   486
GAA TTT ATA GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GGA GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GCC CAA ATG GAG GAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN (Fig. 17-HH)

```
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTGGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTGTGTCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGGAGGA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTTCGCAGT CTGTACCCTT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GGCTATTAAA AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GTACTCGAAG GAATGTGCTG ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGGCTATATG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA AATACCCGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTGTA AGATGTTGTA CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGGATTAC AGGACTACAA AGCCATTGGC ACCGGGCCACA 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCAGAGAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
```

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT  120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA  180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT  480
AGTTATGCCG ATGAXGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA  600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT  780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT  840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAAATTAGAG CAGAGGAAAT TGCCGCTATA  900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGGAAGA TGCTAGGGCA  960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACTACTA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGGCT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTTGTTGTTA AAAGACGCTA TTGGAGTGAG 1860
```

ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GGAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTGTTGTA AGATGTTTGTA GAGAGAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGGAGC GGAAAGATAA GCGAATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTC TTT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAG AGT GTT GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA GAC ACC TTA ATA   270
CTC AAG AAA GGA GAA AAG TTC TTA AAG ATA ACA ATT CAA AAG GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG ATG GAG GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GAA GTC CTA AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT AGC ATA TTT ATT GCC GAA AAT   486
GAA TTT ATA ATG AAG GCA GAA ACC CAG GAG GTT GAG ACA ATA ACT   540
CTT GAA GAT GGA TTA GAC ATC GAA GTT CAA GAG ACA AAG AGC GCA   594
TAT ACA GTC AGC TAT GGA CAT ATG AAA GGA CTT GAG AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GTT CCC ATG CAA ATG GAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

<u>Deep Vent- (PCNA) DNA polymerase fusion protein</u> (Fig. 17-II)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG   60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACGCCCGA GAGGCCATGG   180
AAGATAGTGA GAATTATAGA TGCCGGAAAG GTAAGGAAGA AGTTCCTGGG GGATAAGATA   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CGCAATAAG GGATAAGATA   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360

Fig. 17 II (cont')

```
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAACGTGGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC    780
TACCAGGTGA TTAGGAGAAC GATAAACCTC CCAACAATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGGATGCAAA GGGCCTGGGAG   900
ACTGGAAAGG GGGAGTTCTT CCCAAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC   960
GAGCTCGGTA GGGAGTTCTT TTCAAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG  1020
CTGTGGGATG TTTCTAGGTC TTCAAACTGGC AAGCCGGATG AGAGGGAGTA CGGAGAAGG   1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGGAGAAGG    1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG   1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA   1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC   1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT   1440
GATTACAGGC AACGGGCAAT CAAAAATCCTG GCAAACAGCT ATTATGGGTA TTAGTGGGTAC 1500
GCAAAAGCCC GTTGGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA   1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC   1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG   1800
GAAGGGGAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA AGGCTCAAGT CGAAAATAGCC 1860
AAAGAAACCC AAGCAGAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA  1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGGACCAAGT ACGAAAATACC TCCAGAAAAG  1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC  2040
GTTGCGGTGG CAAAAAGGTT AGCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGGCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTTACCT  2220
GCCGTTCTTA GAATATTAGA GGCCTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG    2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //                2328
```

```
//  ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
    ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
    AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT AGA GTT GAC CTA AAT CTC CCG       162
    TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
```

(PCNA) - Deep Vent DNA polymerase fusion protein (Fig. 17-JJ)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA AAG GAC ACC TTA ATA    270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAT ATT CAA AAG GAC CTC GCA ACA    324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAG ATG GAG ACT GCA ACA        378
GAA CTT CCA TTC GCA AAG GTT CTT GGA GAG GTT GAC CTC CCA                432
GTT AAA GAT GCC TCT CTA GTG AGT ATA AAA TTT ATT GCC AGG AAT            486
GAA TTT ATA ATG AAG GCA ACC CAG GAA GTT GAG ATA AAG CTA ACT            540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAA GTT CAA GAA GTT GAG ACA AGC GCA  594
TAT GGA GTC AGC TAT GGA GTT GAG CTT GGA GAG ACA AAG GCC GAT GAA         648
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAG GAG TAT TAC ATT AGA  702
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA GAT AGA GCC GCG TTT ACA GAA GAT GGG ATA              108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT CCA GTT AGA GAT GTT GTT CTC GTT AAC          216
ATG GAC CAC CTA AAG GAG ATC CTA AAG GTT GAG ATA AAG GTT TTA ATA          270
CTC AAG AAA GGA GAA AAC TTC TTA AAG GAA ATT CAA AAG GAC ACA              324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTT GAA ATG GAG ACT GCA ACA          378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GGA GAG GTT GAC CTC CCA              432
GTT AAA GAT GCC TCT CTA GTG AGT ATA AAA TTT ATT GCC AGG AAT             486
GAA TTT ATA ATG AAG GCA ACC CAG GAA GTT GAG ATA AAG CTA ACT             540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAA GTT CAA GAA GTT GAG ACA AGC GCA  594
TAT GGA GTC AGC TAT GGA GTT GAG CTT GGA GAG ACA AAG GCC GAT GAA         648
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //          702
```

```
//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAACG  GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT      120
```

```
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT    240
GAGGTATGGA GGCTGTTACT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT    420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC    540
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATTGAG   600
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG    660
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT    720
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGGACGGTAG TGAGCCAAAG   780
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC    840
GAGCTCGGTA TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG    900
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG    960
GCCTACGAGA GGAATGAATT AAGCCGGATG AGAAAGGGCT CTGGGAGGGG               1020
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCCG GAGAAAGGGCT CTGGGAGGGG   1080
TTAGTTTCCC TAGATTTCAG GAGCCTGATAA TAATCACCCA TAACGTCTCA              1140
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC    1200
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA    1260
AGGCCAGGAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT    1320
ACTGGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAAATGG AGGATGCAAA GGTAACGTAC   1380
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT CAATCGAGAA GAAGATGCTT    1440
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG ATTATGGGTA TTATGGGTAC    1500
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG TTACGGCCTG GGGGAGGGAA    1560
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT CTTATACATA    1620
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGTTCAAAGT AAAGAAGAAA    1680
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGGAAGAAG AGTATGCGTT GATAGATGAG    1740
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC    1800
AAAGAAACCC CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA               1860
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG    1920
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC    1980
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA    2040
GGGTACATAG TGCTGAGGGG AGACGGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2100
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT    2160
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG    2220
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA                2328
```

JDF-3 – (PCNA) fusion protein (Fig. 17-KK)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGAATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTTCTTCAAGAAGGAGGAACGGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAACCGCGGGAAGAGAATAACCGCGGAGGCGCAGGGTCGTTAAGGTTAAGCGCGGAAGGTGAAGAAAGTTCCTCGG
CAGGTCGTTGGGAGGTCTTGGGTGGTTCCTCTTCACGCACCCGGTCAATCCGCGACAAAATAAGGAAGCACCCCGTCATCGAACTACAGGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAAGGCTAATCCGATGAAGGTGAGGAAGAGCTTAAACTCATGTCTT[GAG][ATC][GAG]ACGCTTCTACCACGAGGGGAGGAAGAGAGTTTGGAA
CCGGGGCCGATTCTGATGAATAAGCTACGCCGATGAAAGCGAGGCGGCGGTGATAACTGGAAGAAGAATCGAACTCATGTCTTCCTTACGTTGAGGTTGTTCTCCACCGAGAAGAGGAA
GCGCTTCTTGAGGGTCGTTAAGGAGGAAGGACCCGGACGTGCTGATAACATCAACGGCGACCTTCCTTGGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCCTCGGGAGGGAGGGAGCGGAGCCGAAGATACAGCGCATGGGACGTTTGCCGTTGCGCTCAAGCGACCAGGTTCGGTTCTATCCAGTTCATAAGGCGCACCATAA
ACCTCCGACCTACACCCTTGAGGCTTTTTCGGAGGAAGGTTCTACGGCAAGGAGGAGTCTAGCCGCCGAGGATAGCCACCGGCCTGGGAGACGCGGCGAGGGGGCTTGAGAG
GGTCGCGCGCGCTACTCGATGGAGGGGTTAACTCGACGGTTACTTCGGCCAAGCCCAAGAAGTCTACGGCAGGAGGCTAAGAGAGGGGAAAAGCGGGAGAGAGAGTTTGAGAG
ACgcCGGTGGCTACGTCAAGGGACCGGAGCCGGTGGTTCCTCCTAAGGAAGGCCTACGAGGGGAACTTCATATCGTGTTATCTAGACTTTCGTTAGTCCAACAAGCGCCC[CCT]TCAATCATAATCACCCACGAGGGTCTCGCCGAGATAC
GCTCAACCGCGAGGGGTGTAGGGACTGTTGGGGGGACTGTTCCTCCTAAGGAAGGCCTACGAGGGGAACTTCTTCCCGAATTCTGCGAAAGCCTCGTCGGAAACCTGCTGGAGAAAGG
CAGAAGATAAAGAGGAAGAAAGATGAAGGCAACTCTCGACGTTGCCCCGGCGTTACGGAGAAGAATCTCCTCGATTACAGGACGAACGCCGCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTCGCGCCGAGAGCCGTTACGGAGAAGAATACATCGGGAAGTACATCTGAAATGGGACTTGAGGAAGCTTGAGGAAAGAAGTTCGGGTTTTAAAGTCCT
CTATGCAGACACAGGTCTCCATGCCACCATTCCTGAAGCTGAACGCTGAAGAAAATGGAGTTCTTAAACTATATCAAATCCCAAACTGCCCGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGGCGGAAGAAAAGTACCGCGGTCAGTCATCGACGGAGGCAAGATAAACACGCGCGCGGGCCTTGAGATAGTCAGGCGG
ACTGGAGCGAGATAGCGAAGGGACGACGAGGGGTTTGGAGGCGGTTGTTGACGGGTTTATCCACGAGATTGTCACGGGAAAGCTGAGCAA
GTTAAAATCCGGCCCGGAGAACTGTTGATAAGCTTTATCCACGAGCAGATAACTACTACGGTGACCGGGTCTCGAGAATTGTCACGAGAAAGCTGAGCGA
GTACGAGGTTCGCGCCGGAGAAGCTGGTTATCGTTCTGCCGGGAATAGGGCTCAAGGGGCGATTCCCTTGACGGAGTTCGACCGGAAGCGTTTGGCGCCGCAGAGGT
CGGACTACATCGAGAACCAGGTTCTGCCGGGAATCCTCAGGGGCCTTCGGCTACCGCAAGGAAGACGAGGCAGGTCGCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC     54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT ACA GAA GAT GGG ATA          108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG  162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT CCA ACA ATT GGA GTT AAC          216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GCA AAG GAC ACC TTA ATA          270
CTC AAG GAC GAA AAC TTC TTA GAG ATA ATT CAA GGA GAC GCA ACA              324
AGA ACA TTT AGA GGA GTT CCC CTA ATA GAT GTA GAG ATG GAA GTT GAC CTC CCA  378
GAA CTT CCA TTC ACT GCA AAG GTT CTT GGA GAG GTC CTA AAA GAT GCT          432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT  486
```

GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GAG GGA TTA TTG GAC GTT CAA GAG ACA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG GAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

(PCNA) - JDF-3 fusion protein (Fig. 17-LL)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTC ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AGA ATC CTA AAG AGA GGT AAA ACC TTA ATA   270
CTC AAG AAA GGA GAA AAG TTC TTA GAG ATA ATT CAA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GTT CTT GAA GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTA GTT CTT GAA GTC CTA AAA GCT   432
GTT AAA GAT TCT CTA GTG AGT GTT ATA AAA TTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GCA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GAG GGA TTA TTG GAC GTT CAA GAG ACA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG GAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTGTCTTCAAGATGTTCAGGATTGAATACGACGAGTTCGAG
CCCTACTTCTACGCCTCCTCAGGGACGACTCTGCCATCGAGAGAAAATCAAAAGATAACCGGGAGAAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGCGAGAAGGT
GAAGAAAAGTTCCTCGGCAGGTCTGTGTGGAGGTCTGGGTCTGCCATGAGTCCTACTCCTCTACTTCACGCCACAGCCCAGXXXCCGGGCAATCCGGACAAAAATAAGAAGCACCCGCGGGTCA
TCGACATCTACGAGTACGACACATACCCTTCGCCAAGCGCTACCTCATCATGAACAAGGGCTACCACCCGAGACTTCCAGTCATAAGGGTCATTTATCCTCGGGACGCGGAGAAGATCAAGCT
GAG ACGCTCTACCACGAGGGAGGAGAGTTTGGAACGGGACCGATTCTGATGATTAAGCTACGCGATGAAAGCGAGGGCGCGTGTAACCTGGAAGAGAAGATCAAGCTGACATC
TCCTTACGTTGAGGTTGTGTCTCCACCGAGAAGGAGAAGTTTGGAGGTTCGTTGATAACATACAACGGCGACAACT
TCGACTTCGCCTACTTGAAATGCGCTCGAGAAGATACGAGTGCCATGAGCGCCAGGGTCACTTGAACAGGCGATACAGCGCATGGGGGGACAGGTTTGCG
GTCGAGGGTGAAGGGCAGGGGTACAAAAGCGCTTTATCCAGTCATAAGGCTTTGGCGTCGTTGATTAAGCTACGCGATGAAAGCGAGGGCGCGTGTAACCTGGAAGAGATCAAGCT
GCCCAAGGAGAAGGTCTACGGCGGGTACAGCGAGGAGATAGCCACGGCACCGCTGGGCGCTCCAGCCTTTGGCTCATCGGCGGCGCGCTACTCGATGGGAAGGCGGGGTTTTTCGGCAA
AGTTGGCAGGAGGGAGTTCTTCCGGCCAGGGATGGGAGGACAACCTCGACACCACGGCGAGGTCGCGAGGGGTTACCTACG
CTCCTAAGGAGAAGGCCTACGAGGAGGAACGAACTCGCCTCCAACAGCCCGACGACTGGGCTGGGCTACGCCGGTGGCTACGTCGACGTCAAGGAGGAGCC

Fig. 17 LL (cont)

GGAGCGGGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAC[CCT]TCAATCATATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGT
GTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCGCGCTTCATTCCGAGCCTGCTTGCTGGAAACCTGCTGGAGGAAAGGCAGAAGATA
AAGAGGAAGAATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACACAGGCAACG[GC]ATCAAGATTCTCGCCACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGAATGGTTACTGCAGGGAGTGCCCGAGGGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCGAGAGAGCTTGAGGAAAAGTTCGGTTTTA
AAGTCCTCTATGCAGACATCAGAGACGGGTCTCCATGCCACCATTCCTGGAGCGGCTGAAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAA
CTGCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTTCGTCACGGGGGGGCGATACTCAGGCGTTGAGGGCAGATGGGGTCATCGACGAGGAGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGGTTTTGGAGGGTGTTATCCACGAGCAGATAACGCCGGAGGGCTCCGGAAGGATAGGCGGACAG
TTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGAGAAGCTGGTTAAAATCCGGCCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGGACAG
CCGCACGTAGCCATAGCGAAGCGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGGACAG
GGCGATTCCTTCGACCCGACGAGCAACAAGTACGATGGGGACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGCGCCTTCG
GCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGGCTTGGGCGTGGGCTGA

<u>Sac7d gene (ACCESSION No: M87569) (Fig. 17-MM)</u>

```
M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA    18

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC    36

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA    54

L   D   M   L   A   R   A   E   R   E   K   K   *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA TAA                        67
```

<u>Sac7d-Taq DNA polymerase fusion protein (Fig. 17-NN)</u>

```
M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA    54

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC    108

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA    162

L   D   M   L   A   R   A   E   R   E   K   K
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA                            201

G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
```

Fig. 17 NN (cont)

```
S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTC GTG TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTC GTC GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC GTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   L   L   K   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG CTG CTG AAG GAG TGG GGC AGC CTG GAA

A   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L   L
GCC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
```

Fig. 17 NN (cont)

```
      CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R  A  F  L  E  R  L  E  F  G  S  L  H  E  F  G  L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT
L  E  S  P  K  A  L  E  E  A  P  W  P  P  E  G  A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCG CCG GAA GGG GCC
F  V  G  F  V  L  S  R  K  E  P  M  W  A  D  L  A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTG GCC
L  A  A  R  G  G  R  V  H  R  A  P  E  P  Y  K  A
CTG GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L  R  D  L  K  E  A  R  G  L  P  G  D  P  M  L  A
CTC AGG GAC CTG AAG GAG GCG CGG CTT CCC GGG GAC CCC ATG CTC CTG
A  L  R  E  G  L  G  L  P  P  G  V  A  R  R  Y  G
GCC CTG AGG GAA GGC CTG CCG CCC GGG GTG GAC CGG CGC TAC GGC
Y  L  L  D  P  S  N  T  T  P  E  G  D  D  L  S  V  L
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GAC GAC CTC AGC GTT CTG
G  E  W  T  E  E  A  G  E  R  A  A  L  S  E  R  L  F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GCC CTT TCC GAG AGG CTC TTC
A  N  L  W  G  R  L  E  G  E  E  R  L  L  W  L  Y  R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E  V  E  R  P  L  S  A  V  L  A  H  M  E  A  T  G  V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R  L  D  V  A  Y  L  R  A  L  S  L  E  V  A  E  E  I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG ATC
A  R  L  E  A  E  V  F  R  L  A  G  H  P  F  N  L  N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
```

Fig. 17 NN (con't)

```
 S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

 L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCG TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G   R   L   H   T   R   F   N   Q   T   A   T   I   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG ATC GGC AGG CTA AGT

 S   S   D   P   N   L   Q   N   I   P   V   R   T   P   L   G   Q   R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I   R   R   A   F   I   A   E   E   G   W   L   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S   Q   I   E   L   R   V   L   A   H   L   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R   V   F   Q   E   G   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG CGG GCG AAG ACC ATC

 N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC
```

Taq DNA polymerase- Sac7d fusion protein (Fig. 17-OO)

```
 V   E   T   L   F   G   R   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCC GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGG

 T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

 E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

 P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCA GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

 V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

 L   S   A   K   E   G   I   D   G   R   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGG GGC GGG CAT CAT CAT

 H   H   *
CAT CAT TAA

 G   G   G
// GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

 D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
```

Fig. 1700 (cont)

```
S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGG CGG GCC CCA ACG CCG

E   D   F   P   R   Q   L   A   L   I   K   E   L   A   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GCG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTG CTG GCC AGC CTG

A   K   K   A   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

D   L   Y   Q   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

G   I   G   E   K   T   A   R   K   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT GAG GAG TGG GGG AGC CTG GAA

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

A   L   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   E   P   D   R   E   R   L
CTC CCG CTG GAG GTC GAC TTC GCC AAG CGC GAG CCC GAC CGC GAG CGC CTG
```

114/186

Fig. 17 00 (cont)

```
                CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG GAG GAG CCC GAC CGG GAG AGG CTT

 R   F   L   E   R   L   E   F   G   S   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

 L   E   S   P   K   A   L   E   E   A   P   W   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCG CCG GAA GGG GCC

 F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

 L   A   A   R   G   G   R   V   H   R   E   P   Y   K   A
CTG GCC GCC AGG GGG GGC CGG GTC CAC CGG GAG CCC TAT AAA GCC

 L   R   D   L   K²  E   A   G   L   L   A   K   D   L   S   V   L
CTC AGG GAC CTG AAG GAG GCG CTT GGC CTC GCC AAA GAC CTG AGC GTT CTG

 A   L   R   E   G   L   G   L   P   P   G   D   D   P   M   L   A
GCC CTG AGG GAA GGC CTC GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

 Y   L   D   P   S   N   T   T   P   E   G   V   A   R   R   Y   G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

 G   E   W   T   E   E   A   G   E   R   A   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCG GCC CTT TCC GAG AGG CTC TTC

 A   N   L   W   G   R   L   E   G   E   R   A   L   S   L   W   L   Y   R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG CGG GCC CTC CTG TGG CTT TAC CGG

 E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG ACG GGG GTG

 R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

 A   R   L   E   A   E   V   F   R   L   A   G   H   P   F   N   L   N
GCC CGC CTG GAG GCC GAG GTC TTC CGC CTG GCA GGG CAC CCC TTC AAC CTC AAC
```

Fig. 1700 (cont)

```
S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC AGC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S   S   D   P   N   L   R   I   A   E   G   W   L   V   A   L   D   Y
AGC TCC GAT CCC AAC CTC AGG ATC GCC GAG GGG TGG CTA GTG GCC CTG GAC TAT

I   R   R   A   F   I   A   E   E   G   N   L   I
ATC CGG CGG GCC TTC ATC GCC GAG GAG GGG AAC CTG ATC

S   Q   I   E   L   R   V   L   A   H   L   S   G   D   E   N   L
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG

R   V   F   Q   E   G   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC
```

Fig. 1700 (cont.)

```
V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   E   R   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCG GCC GAG CGC AAC ATG CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   A   F   N   M   P   V   Q   G
ACC GCC GAC CTC ATG AAG CTG GCT ATG GCC TTC AAC ATG CCC GTC CAG GGC

E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTC GTC CTC GAG GCC

P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG ATT GAT GGC CGC GGC GGA GGG CAT CAT CAT

V   Y   P   L   A   V   P   L   E   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

H   H   //  //
CAT CAT  //  //

M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GTA GAC ACT TCA

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

L   D   M   L   A   R   A   E   R   E   K   K   //  //  *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA  //  //  TAG
```

Pfu DNA Polymerase (WT)-Sac7d fusion protein (Fig. 17-PP)

//

```
ccctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaag ttattctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgatte
aaagattgag gaagttaaga aaataacggg ggaaaggcat ggaaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagtaatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgatcaaga gattctcag gaataggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
```

Fig 17 PP (cont)

```
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
cccttccaatg gaaattcaag tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc caagaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaagg caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac aagtacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaaggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaagaa aagtcattac
tcgtggttta gagatagtta ggagagaatg gagtgaaatt gcaaaagaaa ctcaagctag
```

```
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacaactc aaaattgttt tgtctcattt
taactttac agaaataact gtctcaaatt atgacaactc ttgacaactt tacttcatta
```

ccagggtaat gttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggttgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttccttgg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT GTA GAC GAC
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Sac7d - Pfu DNA Polymerase (WT) fusion protein (Fig. 17-QQ)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT GTA GAC GAC
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
//

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtgggggagc ataatgatt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa ctttagagcc atacattac gctcttctca gggatgatc

```
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaactta
tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcaag gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagagagaat acattcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaatt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
cctccaatg gaaattcaag tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcacac
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatcccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
```

fig. 17 6a (cont)

```
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggaaga aagtacacg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaaggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaagaa aagtcattac
tccgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agtttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaaagc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc caaaaaagca
caagtatgac gcagaatatt acattgagaa cagataccaa aagacaagac ttaggatatt
ggagggatt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
```

123/186

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacaattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctaact

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taacttttac agaaataact gttctcaaatt atgacaattt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagaacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgtcttgg // TGA

<u>Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein</u> (Fig. 17-RR)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GTG AAG GTA AAG TTC AAG TAT GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATGAAGA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG ATGATTCAAA GATTGAAGAA ACCGTGTTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT CAAGCCTATT 240 ACCGTGTTGA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG GAATTAAATTA ACCATTGGAA GAGATGGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAAATTTTG GAAAGCCAAA GGGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCAGGGG AAGAGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCAACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGGAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG
TGGATTCGTT AAAAGAGCCAG AGAAGGGGTT GGGGAAAAC 1200 ATAGTATACC TAGATTTGA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGGACATTT GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGGAGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTTCTT 1440 GACTATAGAC AAAAAGCGAT GTTACTGCCG AAAACTCTTA GCAAATTCTT TCTACGGGATA TTATGGCTAT 1500
GCAAAAGCAA AATACTCCTT 1620 GACACTGATG GTTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGGAAT AAAGAAAAAG
GAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGGAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCAATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACACAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGCGCTAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA
2328

PFU DNA POLYMERASE (V93 R OR E)-Sac7d fusion protein (Fig. 17-SS)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTACGCT 120 CTTCTCAGGG ATGATGAAGA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTTGGA AACTTTATTT GGAACATCCC

CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360

CTCATCGACA AAGGCCTAAT ACCAAGTGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA

GAGTTTGGAA AAGGCCCAAT TATAATGATT AGTTATGCAG ATGAAAATGA AGCAAAGGTG 480 ATTACTTGGA AAAAACATAGA TCTTCCATAC 540

GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATATT TACTTATAAT

GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGAAG GAGAGCCAAG CGAGCCCAAG 720

ATGCAGAGAA TAGGCGATAT GACGGCGTGTA GAAGTCAAGG GAAGAAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AGCCTGGGAA

CCAACATACA CACTAGAGGC TGTAGGATGA 840 GCAATTTTTG GAAAGCCAAA TACGCCGACG AGATAGCGAAA AGCCTGGGAA 900

AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCCGATG AAGATGCAAA GGAGAAGGTA 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA

ATTCAGCTTT CAAGATTAGT TGGACAAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA

1080 GCCTACGAAG GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG

TGGATTCGTT AAAGAGCCAG AAAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA

CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA

AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC

CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500

GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGACCG TTACTGCTGG AAGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGGAGCTCGAA

GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA AAAGGAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAAATAT 1740 GAAGGGTTTT ATAAGAGGGG

ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG

TGAAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGAAGCT 1920 GTGAGAATAG

TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980 CTCGCAATAT AACAAGACCA TTACATGAGT

ATAAAGCCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA TAAAGCCAGG AATGGTAATT 2100

GGGATACATAG TACTTAGAGG CGATGGTCCA AATTAGCAATA GGGCAAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA

GAATAATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAG

2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG GGT GAA GAG GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA GAG GAG AAG AAA // TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-Sac7d fusion protein (Fig. 17-TT)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAAATGATT 480 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAG 600 AAGGATCCTG ACATTTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AGCCTGGGAA AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAG AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCCGATG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
AATCAGCTTT CAAGATTAGT TGGACAAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCCGATACTC TAAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGACGG TTACTGCTGC GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCCTCACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTTGAGGGAAAT AAAGAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980 CTCGCAAATAT ATGAGCAGAT AACAAGACCA TTTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACAATA TACTTAGGAG CGATGGGTCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
2328

PFU DNA POLYMERASE (G387P/V93R OR E)-Sac7d fusion protein(Fig. 17-UU)

// ATG GTG AAG GTA AAG TTC AAG TAT GGT GAA GAG AAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GCT GTA AGC GTA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG GAG AAG AAA // TGA

Fig. 1700 (cont)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATCAAG GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATGCGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAAATGGAG GGGGAAGAAG AGCTAAAGTG TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAATTTAGCG 660 AAAAGGGCAG AAAAAACTGG TATCAGGGAG AGCCCAAG 720
GGAGACTCAT TCGGCATTCC ATATTTAGCG 660 AAAAGGGCAG TTCTCAGGAT TATCAGGGAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGGAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCAGATT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGGAA
1080 GCCTACGAAG GAAACGAAGT AGCTCCAAGC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGGAGA GCTACACACC
NGGATTCGTT AAAGAGCCAG AAAAGGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA
CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACAATCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAACAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCCT 1440 GACTATAGAC AAAAAGCGAT GCAAATTCTT TCTACGGATA TTAATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGAGCTCGAA
GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAGAGAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTGTTG AATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //

2328

// ATG GTG AAG GTA AAG TTC AAG GGT GAA GAA GTA GAC TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GCA GGA GCT GTA AGC GAA AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA AGA GAG GAG AAG AAA // TGA

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA GCA GAA AGA GAG GAG AAG GAA TTA //
```

```
//ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA.CATTACGCT 120 CTTCTGAGGG ATGATGAAGA GTTAAGAGAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGGAAG AGTTCTCAGG ATGATTCAAA GATTGAAGAA 240 ACCGTGTGGA AAACTTTATT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC TTCCATTTGC AAAAGAATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGTAGCAGAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA
GCTACACAGG.TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT 1260 CCGATACTC TAAATCTTGA GGGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGCCGCC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT GTTACTGCTG GGAAGAGAAG AAAAACTCTTA TTATGGCTAT
1500 GCAAAAGCAA GATGGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560 TACATCGAGT TAGTATGGAA
GGAGCTCGAA GAAAAGTTTG GATTTAAAGT TAAGGAGTGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA
AAAGAAAAAG 1680 GCTCCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGTTAGA GACTGAAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG GAAGGAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ACGGAAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAGAG CTTGCCAATT ATGAAGTTCC ATGAAGCAGAT ATGAGGCAGAT AACAAGACCA
TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT ACCAGAAACT AGCTGCTAAA TAAAGCCAGG AATGGTAATT
2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACA
```

GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

<u>KOD DNA POLYMERASE - Sac7d fusion protein</u> (Fig. 17-WW)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC  120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG  180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGGCGATAAG GGACAAGATA  300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGGGCTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAAACGGCT AGAACGTGGA TCTCCCCTAC  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG TCCTCGCGTT CTATCTGAAA TGTGAAGGAG  600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA  660
AAGCGCTGTG AAATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG CGAGCCGAAG  720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA  840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCGAGG AAATAACCAC AGCCTGGGAA  900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC  960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA CGTCCTGCCG CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG TCGAGGAGAA GCTCCTCGAT CGGCTATGCA 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA AAGTACGGGTAC           1560
ATAACGAATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AAATACCTGGA GCCGATGCTG AAAGAAGGCT           1680
```

130/186

ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGAATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGACGTGG CGGACGAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC CCGGAAGGGAA CT 2325

Sac7d - ROD DNA POLYMERASE fusion protein (Fig. 17-XX)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG AGTTCCTCGG GAGAGCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGGATAAG GGACAAGATA 300
CGGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600

```
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGGAA CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAAACTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCCAGTCC 1020
CTCTGGGACG TCTCCGGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
TTCTGCAAGG ACTTCCACAG ATTTATCCCG AGCCTGCTTG CCCACAGGT CGGCCACCGC 1320
GATACGCTCA ACAGAAGAGG ATGCAAGGAA TATGACGTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGGTCA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGCAACCGG TCCCCACGTT 2040
GCCGGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGGACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGACAGC CTTCGGGTTAC CGCAAGGAAG ACCTGGCCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325
```

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-YY)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

Fig 17.44 (cont)

```
AAG ATA AAG AAG GTT TGG AGA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA GAG AAG AAG AAA //
```

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT  120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA  180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTAGTCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT  480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG TTGATTTGCC GTATCTCATA              600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGGTGAAA TCAAGGGTAG AATCCACTTT  780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT  840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC CAGAGGAAAT CAATTAGGAG TGCCGCTATA  900
TGGGAAACAG AAGAAAGCAT GCCCAGTACT CAATGGAAGA GCTGATAGGT              960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA             1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTATTCCT CCATACTCGG GGACTTAATT             1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAAGTGCTG  AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAA  AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGGATTAA AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
```

CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACAATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN (Fig. 17-ZZ)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGAC XXX C CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGGAGAA TGAACTTGCA CCGGAACAAAC CTGATGAGGA AGAGTAATAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCGGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTATA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGGAA GAAGTGTGCTG AAAGCGTTAC CGCAGGCGGGG 1560
AGACACTACA TAGAGGATGAC ATAGAGGAAA AGTTCGGGCTT TAAGGTTCTT 1620

TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGAATT TTTGTTACAA AAAAGGCGTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTGTTGTA AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGGAG GGAAAGATAA GCGGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA GCA GAA AGA GAG AAG AAA // TGA

Deep Vent- Sac7d DNA polymerase fusion protein (Fig. 17-AAA)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACGCCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGGAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GAGTTGGCGA AGGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACACAC GGCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840

Fig. 17 AAA (con't)

```
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG  900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC  960
GAGCTCGGTA GGGAGTTCTT CCCAAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGGCTGG GGGATACGTT AAGGAGCCCG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC AGGGTTTATC CCCAGCCTGC TCAAGGACCC GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGGACCC ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTTGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCGCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //              2328
```

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA
```

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA GCA GAA AGA GAG GAG AAG AAA //
```

```
//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT     120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT    240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGGCAATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
CTAATAGACA AAGGCCTAAT TCCAAATGGA AGGCGATGAAG AGCTCAAGTT GCTCGGCATTT  420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGGCGA AGGGGCCCAT TATAAGGTGGA  480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAACGTGGA AAAAGATCGA TCTCCCGTAC  540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAAGCGGT TCCTCAAGGT GATAAGGGAG  600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT CGACCTTCCC TATCTAGTT    660
AAGAGGGCCG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG CTTTGACCTC   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGAATACA CCCTCGAGGC AGTTTATGAG    780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGAGTTCTT CCCCAGCTTT CAAGGTTAGT CGGCCCAGCCC             1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG   1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG   1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG   1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA   1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC   1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA   1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT   1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC   1500
```

```
GCAAAAGCCC GTTGGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA   1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA   1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA   1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC   1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCCGTT GATAGATGAG   1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC   1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA   1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG   1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC   2040
GTTGCCGGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT   2220
GCCGTTCTTA GAATATTAGA GGGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA               2328
```

JDF-3 - Sac7d fusion protein (Fig. 17-CCC)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCACTCAGGGTGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACACCGGCGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGAACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGAGCCAGGGTCGTTAAGGTTAAGGCGCGGGAGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCGTTGGAGGTCTGGGTCCTCTACTTCACGCACCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGGGTCATCGAACATCTACGAGTTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCCTAATCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTGGAACGCTCTACCACGAGGGAGAAGAGTTTGGAA
CCGGGCGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGTGCTCAGAGTACTGATAACTTCGCCTTCCTTCGTTGAGGTTGTCTCCACGAGAAGGAGGATGATTAA
GGCGCTTCTTGAGGGTCGTTAAGGAGGAACCCGGACGTGCTGAATAACATACAACGGCGACAACTTCGCCTACCTGAAAAAGCGCTTGGCGTGAGCTTT
ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCCAGGTTTCGGTGAGGTGAAGGGCTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCCGACCTACACCCCTTGAGGCGGTTACTCAGAGGCTTGGCCAAGCCCAAGAAGGTCTACGCCCAGGAGATAGCCACCGCGGCCCGCGAGGGGCTTGAGAG
GGTGCGGCGCGCTACTCGATGGAAGGGGTTACCTCGTTCCTCTACGAGGCTTGGCAAGGGCCAAGCCTTCCAGGGCTCATCGGCCTGGGAGAACGGCGAGGGGCGACGTTTCC
CGCTCCAGCACCGGCCACTCGTCGTCGAGTGGTTCCTCTTAAGGAAGCCCTACGAGGAGTTCTTCCCGATGGAGAAGCTTCCAGGCGTCATCGGACCTTTATCCAGTCATAAGG
ACGcGCGGTGGCTACGTCAAGGAGCGGGGGCGAGGGGGACTGTGGGGACAATATCGTTGCTCAGGAGGAGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGGCGAGGAGAAGGGGGCT
GCTCAACCGCGCGAGGGGCTACGTGCCCCGAGGTCGGTCACAATATCGTTGTTCTGCAAGAACTTCCCGGCTTCATTCCCGGCAAACGCTCTGGGAGGAAAGG
CAGAAGATAAAGAGGAAGAATGAAGGCAACTCTCGACCGCGGAGAAGAATCTCCTCGATTACAGGCAACGGcGCCTTCAATCATAATCACCCACACAGTCTCGCGAGATAC
ATGCCAGGGGCAAGAATGGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCCATGGGGAAGGAGTACATCGAAAAGTTCGGTTTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGACGGCGGACGCTCAAGGAGTTCTTAACTATATCAATCCCAAATCCCGGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGGCGAAAAAGTACGCGGTCATCAGAATGTTCAGGAGGAAGTTCGGTTTTTAAAGTGTCT
CAGAAGATAAAGAGGAAGAATGAAGGCAACTCTCGACCGCGGAGAAGAATCTCCTCGATTACAGGCAACGGcGCCTTC
GTACGGAGGTTCCGCCGGGATAGCGAGGGGTATCGCCGAGACTCAAGGACTACAAGGCAGTTAGCATAGCGAACGACTACAAGGCCCACGCGCCCGCGCACGTAGCCCATAGCGAAGcGTTTGGCCGCCCAGAGGT
```

GTTAAAATCCGGACCCGGGAACTGTTGATAAGCTACATCGTTCTGTTCGAAGGGATAGGCGACCAGGGCGACGAAGGCGAATCCCTTCGACGAGTTCGACCCGGACGAACGGAGTTGACCGGAGTTCGAACGACCAAGTACGATG
CGGACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTACCGGAACCTGGCGCTACCAGAAGACGAGGCAGGTCGGGGCTTGGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

Sac7d - JDF-3 fusion protein (Fig. 17-DDD)

//ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AGA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGAATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCACTCAGGGGTCTTCAAGAAGGAGAACGGCGAGTTGAATACGACCGCGAGCCCTACTT
CTACGCGCTCCTCAGGGACGACTCTGCCATGGAAAAAAGCAAAAGATAACGGCGGAGCACGACCCCGGAGGTCGTTAAGCGCGGAGGTTGAAGAAAAGTTCCTC
GGCAGGTCTGTGGGAGGTCTTCGGGGTCCTTACTTCACGAAGAAATCCGCGACATCGGAGCGCAAATAAGGAGAACGACCCCGGAGGTCGTTAAGCGCGGAGCTCTACGAGTCTACAGTCGACATAC
CCTTCGGCAAGCGCTACCTCATAGACAAAGGGCCTAATCCCGATGGAAGGCTTAAACTCATGTCCTTGAACGCTCTACCACGAGGGAGGAAGGAGAATGATT
AACCGGCGGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGTGATAAACCTGAAGAAGATCGACCTTCCTTACGTTGAGTTGTCTCCACCGAGAAAGGAGAGATGATT
AAGCGCTTCTTGAGGGTCGTTAAGGAGGACCCGGACGTGCTGATAACATAGAACTTCGACTTCGCCTACCTGAAAAGGCGCTGTGAGAAGCTTGGCGGTGAGCT
TTACCCTCGGGAGGGACCGGGAGCCGAAGAAGGACCATGGGGACTACAGCGAGGTTTGCGCAGGGTTCAGAGACCTCGGAAAAAGGCTGTGAGAAGCTTGGCGGTGAGCT
AAACCTCCCGACCTACACCCCTGAGCGTGTATACGAGGCGGTTTTCGGCAAGCCCAGGAGAGAGATAGCCACGCTGGAGAGGCCCTCGGGGACGTTT
AGGGTCGCGCGCTACTCGATGGAGACGCGAGTGGTTCCTCGTCAGGAGAAGGCTTGGCAAGCAGGTTTGCGCAGGGTTCAGAGACCTCGGAAAAAGGCTGTGAG
CCCGGCTCCAGCAACCTCGTCGAGGAGACGGGGTTCCTCGTCAGGAGGAGGTTCTTCCCGATGGAGGGCCCAGTCTTTCGGCCAGGCTCATCGGCGGACATAAGGCGCGACCAT
CTACgccGGTGGGCTACGTCAAGGAGGACCGGAGCGGGGACTGTGGGACCAATATCGTGTATCTAGACTTTCGTAGTCTTCACCGAGGGAAGGAGGAGGATT
ACGCTCAACCGCGAGGGGTGTAGGGGTGTAGGGACTCGGCTGCCCCGAGGTCGCAATATCGTGTATCTAGACTTTCGTAGTCTTCATTCGAGCCCTGCTCGGAAGGGGAGA
GGCAGAAGATAAAGAGAGAATGGAAGGCAACTCTCGACGTTGCCGCGAGGAGGTTACGGCGAGTCATCGAAAGTGGTCATCACCGAGGGAAGGAGGAGGAT
CTATGCCAGGCAAGATGGTACTGCGGGAGGAGCGTTACGGCGAGTCATCGAAATGGTCATCGAAAGTGGTTTAAAGTC
TCGAACTCGAAATACGAGACAGAGGTCTCCATGCCAGGCGGAGGCTTACGTTCTTAAAGGCAATGGAGTTCTCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTC
CTCTATGCAGAGACACAGAGGTCTCCATGCCAGGCGGAGGCTTACGTTCTTAAAGGCAATGGAGTTCTCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTC
CGACTGGAGCGAGATAGCGAGGAGAGCTTCTCTACGTCCCATGCCAGGCGGCAAGATAACCACGCGCGGGCAAGATAGTCAGGCG
AAGTACGAGGTTCCGCGAGATAACGCGCGGAGAAGCTGGTTATCCACGAGACTACAAGGCCATAGCGAAGCGTTTGGGCCGCCAGAG

GTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACACATCGTTCTGAAGGGCTTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGA
TGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCCAGGTCGGGGCTTGGC
GCGTGGCTGAAGCCGAAGGGGGAAGAAGAAGTGA

Fig. 17 DDD (con't)

Synthetic Sso7d gene: (Fig. 17-EEE)

```
 A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

 I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

 G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

 L   Q   M   L   E   K   Q   K   K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Sso7d-Taq DNA polymerase fusion protein (Fig. 17-FFF)

```
//  A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

 I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

 G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

 L   Q   M   L   E   K   Q   K   K               G   G   G
CTG CAG ATG CTG GAG AAG CAG AAA AAG    //    //  GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC GTG

 D   G   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S   R   G   E   P   V   Q   A   X   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG OTC TAC GGC TTC GCC AAG AGC CTC AAG

 A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGC GAC GCC GTC ATC GTG GTC TTC GAT GCC AAG GCC CCG
```

fig. 17 FFF (cont')

```
    GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTC TTT GAC GCC AAG GCC CCC
S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   P
    TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG CGG GCC CCC ACG CCA
E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
    GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTC GTC GAC CTC CTG GGG
A   K   K   A   E   K   E   G   Y   E   V   A   D   V   L   A   S   L
    GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC GCG GAC GTG CTG GCC AGC CTG
L   A   R   L   E   V   P   G   Y   E   A   D   K
    CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC AAA
D   L   Y   Q   L   S   D   R   I   H   V   L   T   A   D   K
    GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CTC ACC GCC GAC AAA
L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
    CTC ATC ACC CCG GCC TGG CTT GAA GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
    GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
G   I   G   E   K   T   A   R
    GGC ATC GGG GAG AAG ACG GCG AGG
A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
    GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
A   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
    GCC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
    CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R   A   F   L   E   L   G   S   L   H   E   F   G   L
    AGG GCC TTT CTG GAG CTT GGC AGC CTC CAC GAG TTC GGC AGG
L   E   S   P   K   A   L   E   E   A   P   W   P   P   E   G   A
    CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCG TGG CCG CCG GAA GGG GCC
```

14.2./86

Fig. 17 FFF (cont)

```
F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L   A   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
CTG GCC GCC GCC AGG GGC GGG CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L   R   D   L   K   E   A   R   G   L   L   A   K   D   L   S   V   L
CTC AGG GAC CTG AAG GAG GCG CGG GGC CTT CTC GCC AAA GAC CTG AGC GTT CTG

A   L   R   E   G   L   G   L   P   P   G   D   D   P   M   L   A
GCC CTG AGG GAA GGC CTC GGT CTC CCG CCC GGC GAC GAC CCC ATG CTC CTG

Y   L   L   D   P   S   N   T   T   P   E   G   V   A   R   R   Y   G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCG GAG GGG GTG GCC CGG CGC TAC GGC

G   E   W   T   E   E   A   G   E   E   R   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG GGG GAG GAG CGG GCG CTT TCC GAG AGG CTC TTC

A   N   L   W   G   R   L   E   G   E   R   A   H   M   L   Y   R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG CGG GCC CAC ATG CTC TAC CGG

E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
CGC CTG GAC GTC GCC TAT CTC AGG GCC CTG TCC CTG GAG GTG GCC GAG GAG ATC

L   R   E   A   E   V   F   R   L   F   D   E   L   G   L   P   A   I
CTC CGC GAG GCC GAG GTC TTC CGC CTG TTT GAC GAG CTA GGG CTT CCC GCC ATC

A   R   L   E   A   V   F   R   L   A   G   L   S   L   G   H   P   F   N   L   N
GCC CGC CTC GAG GCC GTC TTC CGC CTG GCC GGG GCC CTG TCC CTG GGC CAC CCC TTC AAC CTC AAC

S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC TTC GAC GAG CTA GGG CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   T   S   A   V   L   P   A   I
GGC AAG ACG GAA AGG ACG GGC AAG CGC TCC ACC AGC GCC GTC CTG CCC GCC ATC

L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
```

Fig. 17 FFF (cont)

```
G   R   L   H   T   R   F   N   Q   T   A   T   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S   S   D   P   N   I   P   V   R   T   P   L   G   Q   R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG GGC AGG

I   R   R   A   F   I   A   E   E   G   W   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

R   V   F   Q   E   G   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

S   Q   I   E   L   R   V   L   A   H   L   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG CGG GCC GCC AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   G   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG CGG GGG TAC

V   E   T   L   F   G   R   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCG GAG CGC ATG GCC AAC ATG CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CAG GTC CAC GAC GAG CTC GTC CTG GAG GCC

P   K   E   R   A   E   A   V   R   L   A   K   E   V   M   E   G
GAA
```

CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT

H   H   *
CAT CAT TAA

Pfu DNA Polymerase (WT) -Sso7d fusion protein (Fig. 17-GGG)

//

```
ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc
tctaacctgg gtttatagtga caaatcttcc tccacacacg ttattctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatatagaag
gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aaacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagttct cggcaagcct attaccgtgt ggaaactta
tttggaacat ccccaagatg ttccactat tagagaaaa gttagacagt atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaaggcct
aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
```

fig. 17 GGG (cont)

```
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgatataaga gatttctcag gattatcaag gaagaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccaatg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acattcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcaag tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaaaggt tttataagag
```

Fig. 17 GGG (con't)

```
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctccaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtaggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc gataggtgta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggaggggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaaatggt
ctatctgcat gcttctctgg ctcggaaang gaggattcat aacaacagta tcaaacattct
cagagaattg agaaacatca cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgtctcca gcagagccgc aaccaatggat aacaccctg ttcccgcacc caagtccgct
acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaacctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
```

taactttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgctttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttccttgg //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

GGT GGC AAG GCC CGT GTC GGT GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

CTG CAG ATG CTG GAG AAG CAG AAA AAG   // TGA

PFU DNA POLYMERASE (V93 R OR E)-Sso7d fusion protein (Fig. 17-HHHH)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL POSSIBLE CODONS FOR GLUTAMIC ACID)

ATGATTTTAG AATGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAAATTAA GATAGAGCAT

GATAGAACTT TTAGACCATA CATTTACGCT TGTTAGACAA AGTTTCTCAGG ATGATCAAA GATTGAAGAA GTTAAGAAAA TAACGCATGGA AAGGCATGGA 180

AAGATTGTGA GAATTGTTGA TGTTAGAGAAG GTTGAGAAAG AGTTTCTCAGG ATGGCTTAT ACCGTGTGGA AACTTTATTT GGAACATCCC

CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360

CTCATCGACA AAGGCCTTAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA

GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAAGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540

GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTTATGT TACTTATAAT

GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAACTTGG GATTAAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC

CCAACATACA CACTAGGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGGAAA AGCCTGGGAA 900

AGTGGAGAGA ACCTTAGGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGA AAGAATTCCT TCCAATGGAA

ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTTCTT ACTTAGGGAA

1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAAGGAGTA TCAAAGAAGG 1140 CTCAGGGAGA GCTACACAGG

TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGGATTA TAATTACCCA

CAATGTTTCT 1260 CCCGATACTC TAAAATCTTGA GGGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA

AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAAACTCTTA GCAAATTCTT TCTACGACTA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGGAGCTCGAA
GAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTGAGAATGG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

PFU DNA POLYMERASE (G387P/V93R OR E)-Sso7d fusion protein (Fig. 17-III)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGG ATGATCAAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GATATAGAAA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600 AAGGATCCTG ACATTATAGT TACTTATAAT
GGAGACTCAT TCGCATTCCC ATATTTAGCG 660 AAAAGGGCAG AAAAAACTTGG GATTAAATTA ACCATTGGAA GGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACAATACA CACTAGAGGC TGTATATGAA 840 GCAAATTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGAATGG AAGATGCAAA GGCAACTTAT 960 GAACTCGGGGA AAGAATTCCT TCCAATGGAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGGAA
1080 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG TCAAAGAAGG 1140 CTCAGGGAGA GCTACACACC ACTTAGGAAA
CAATGTTTCT 1260 CCCGATACTC TAAAATCTTGA AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320 AAGTTCTGCA
AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC
CTATAGAAAA AATACTCCTT 1440 GACTATAGAC AAAAAGCGAT AAAAACTCTTA GCAAATTCTT TCTACGACTA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA GGGAGCTCGAA

GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAA GTGAGGAAAT AAAGAAAAG
1680 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT ATAAGAGGGG
ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG
TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GTAGAAATAG
TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAGAGAAG 1980 CTCGCAATAT ATGAGCGAGAT AACAAGACCA TTACATGAGT
ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGGTCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA
GAATATTACA TGGAGAACCA GGTTCTTCCA GCGGTACTTA GGATATTGGA GGGGATTTGGA TACAGAAAAG TCGGCCTAAC TTCCTGGCTT
2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC
2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GGC
GGT GGC AAG ACC GGG CGT GGT GCG GAA AAG GAC GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG   // TGA

PFU DNA POLYMERASE (D141A/E143A/V93R OR E)-Sso7d fusion protein (Fig.17-JJJ)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT
GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGG ATGATGAAAC AGTTGAAGAA GTTAAGAAGA TAACGGCATGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240 ACCGTGTGGA AACTTTATTT GGAACATCCC
CAAGATXXXC CCACTATTAG AGAAAAAGTT 300 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420 GCNATAGCNA CCCTCTATCA CGAAGGAGAA
GAGTTTGGAA AAGGCCCAAT TATAATGATT 480 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAATCATAG TCTTCCATAC 540
CCAACATACA CACTAGAGGC TGTATATGAA GCAATTTTTG GAAAGCCAAA GGAGAAGGTA 600 TACGCCGACG AGATAGCAAA AGCCTGGGAA
GGAGACTCAT TCGCCATTCC ATATTAGCG 660 AAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780 TATCATGTAA TAACAAGGAC AATAAATCTC
CCAACATACA CACTAGAGGC TGTATATGAA 840 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGGATG AAGATGCAAA GGCAACTTAT 960 GAACTGGGGA AAGAATTCCT ACTTAGGAAA
ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA
GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAGAGTA TCAAAGAAGG 1080 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA
TAATTACCCA CAATGTTTCT 1260 CCCGATACTC TAAATCTTGA GGGGTGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTTC TTGGACATTT GTTAGAGGAA 1380 AGACAAAAGA TTAAGACAAA AATGAAGGAA
ACTCAAGATC CTATAGAGAA AATACTCCTT GACTATAGAC AAAAAGCGAT AAAACTCTTA 1440 GCAAATTCTT TCTACGGATA TTATGGCTAT
1500 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560 TACATCGAGT TAGTATGGAA

GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT
AAAGAAAAAG 1680 GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740 GAAGGGTTTT
ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA
GAGATTGGAG TGAAATTGCA 1860 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ACCAGAGAAG 1980 CTCGCAAATAT ATGAGCAGAT AACAAGACCA
TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AAATGGTAATT
2100 GGATACATAG TACTTAGAGG CGATGGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA
GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG
ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG   // TGA

KOD DNA POLYMERASE - Sso7d fusion protein (Fig. 17-KKK)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGGACGTAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCGGAAG AAATAACCAC AGCCTGGGAA 900
ACGGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAA GCCCAGCTTT CTCGCCAGTCC CGGCCAGTCC 1020
CTCTCGGACG TCTCCCGCTC CAGCAGCTGGC AACCTCGTTG AGTTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGGAGCT GGCCAGAAGA 1140

CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTGA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTAGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAI TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGGC CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GGAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GCCGTTGCCA GAGGGTTGGC CGCGAGAGGA GTCAAAATAC AGGCTAACAC TCCCACGTT 2040
GTGATCCACG AGCAGATAAC GAGGGATTTA AGGGACTACA AGGCAAGTACG GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACGAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CGTTGGCTGAAG CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

Sso7d - KOD DNA POLYMERASE fusion protein (Fig. 17-LLL)

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC CGT GGT GCG GTA AGC GAA GAA GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACGCCCGA GAGGCACGGG 180
ACGGTTGTAA CGGGTTAAGCG GGTTGAAAAG GTTCAGAGAGA AGTTCCTGG GAGACCAGTT 240

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN (Fig. 17-MMM)

```
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGGCGTGTG AAAAGCTCGG AATAAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAAACTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTTCT TCCGGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCGGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGGAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACACAGT CGGCCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGGAGGA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGGCGGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGCCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAAACGG TCCCCACGTT 2040
GCCGGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGCGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT//TAG 2325
```

Fig. 17 MMM (cont)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
  ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
  GGT GGC AAG ACC GGC CGT GGT GTA AGC GAA GAA AAG GAC GCG CCG AAG GAG CTG
  CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT  120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGGA GAGACATGGA  180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAAGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG TTGTTCAAGT GTTATACGCT TGTTAAAGAA  600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT  780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT  840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGAAAT  TGCCGCTATA  900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA  960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC CTGATGAGGA GTATCTTTTA 1080
AGGGTGGCAT ACGCGGAGGA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTACATG 1260
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1320
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1380
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1440
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTTGTTACAA AAAAGCGCTA 1500
GAGTATGAGG GCTTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1560
... ...
DATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG                        1860
```

ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGGATTAC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN (Fig. 17-NNN)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG TTTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAAAT TTGAATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTTGCG AAGGACGATA AACCTCCCAA CGTATGACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC CAGAGGAAAT TGCCGGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA AAAAGAGGGC TGTAAGAATT CAATAAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTTAAGAATT CCATACTCGG GGACTTAATT 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TGTAAGAATT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGATAGGC AATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTTATAAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560

AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGAGAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGGAG GCTTTTACTT GGAGGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGGAG AACAAGGGGC GCAGGATAAC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTTAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Deep Vent- Ssod7 DNA polymerase fusion protein (Fig. 17-000)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACGGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGGAGA TAACGCCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTAIGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CGGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACTTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGGCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAAATCTTG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAAGG GACTGGAGAG TATTGCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGTGGATG TTTCTAGGTC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080

GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCGGT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCGCTGAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGGAGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAACG GAAGATGCTT 1440
GATTACAGGC AACGGCCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTTATGGGTAC 1500
GCAAAAGCCC GTTGGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTCGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGGAGGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CCTAGAGGCT ATCCTAAAGC ATGGCAACGT 1920
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT CTGAGCAAGT ACGAAAATAC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGGGACCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGGTGATA 2100
GGGTACAATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA GGGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCCTTTGGG TACAGGGAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA GAA GAC GCG CCG AAG GAG CTG
CTG CAG ATG AAG CTG GAG AAG CAG AAA AAG // TGA

Ssod7 - Deep Vent DNA polymerase fusion protein (Fig.17-PPP)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA GAA GAC GCG CCG AAG GAG CTG
CTG CAG ATG AAG CTG GAG AAG CAG AAA AAG //

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180

```
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT    240
GAGGTATGGA GGCTGTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT    420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC    540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG    600
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG    660
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTAATCTAGTT    720
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGGTAG TGAGCCAAAG    720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC    780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG    840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC    960
GAGCTCGGTA GGGAGTTCTT CCCAGCTTT CAAGGTTAGT CGGCCAGCCC                1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTGGTTGG AGTGGTACCT CCTCAGGAAG    1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAAG    1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG    1200
TTAGTTTCCC TAGATTTCAG GAGCCGTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA    1260
CCGGATACGC TGAACAGGGA AGGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC    1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA    1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT    1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC    1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA    1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG CTTATACATA                1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA    1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GCTTGAGTAC                1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAGAA AGTATGCGTT GATAGATGAG    1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC    1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAAGGT TGGAGGAGGCA    1920
GTAAAGATAG TTAAGGAGGT CTGAGCAAGT ACGAAATACC TCCAGAAAAG                1980
CTAGTTATTT ACGAGACAGAT CACGAGCGCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC    2040
GTTGCCGTGG CAAAAAGGTT AGCCGGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA    2100
GGGTACATAG TGCTGAGGGG AGACGGGGCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG    2160
TTCGGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT    2220
GCCGTTCTTA GGAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG    2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA                2328
```

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAAGGGCGAGTTCAAGGATTGAATACGACCGCGGAGTTCGAGCCCTACTTCT
ACGGCGTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGGATAACCGCGGAGGCACGCCAGGGTCGTTAAGGTTAAGCTGGAGGAAGAAAAAGTTCCTCGG
CAGGTCTGTGGAGGTCTGGGTCTTCACGCACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGGCGGAGATCTACGAGTTCGACATACCC
TTCGCCAAGCGCTACCTCATAGACACAAAGGGCCTAATCCCGATGGAAGGTGAGGAAGGCTTAAACTCATTGTCCTTTGAGATCGAGCTCTACCACGAGGGGGAGGAGTTTGGAA
GCGGCCGGATTCTGATGAATAAGCTACGCCGGATGAAAGCGAGGGCGCGGCTTAAACTCATTGTCCTTTGAGATCGAGCTCTACCACGAGGGGGAGGAGTTTGGAA
GCGGCTTCTTGAGGGTTCGTTGAAGGAAGAATCGGGACTTCCTTACGGTTGAGTTGTCTCCACCGAGAAGGAGAATGATTAA
ACCTCGGGAGGGGACGGGTGTTAAGGTCAAGATACAGCGCCATGGTGCTGATAACATACAACGCGGTCATCGGCGGAGATCTACGAGTTCGACATACCC
GCGGCTTCTTGAGGGTTCGTTGAAGGAAGAATCGGGACTTCCTTACGGTTGAGTTGTCTCCACCGAGAAGGAGAATGATTAA
ACCTCGGGAGGGGACGGGTGTTAAGGTCAAGATACAGCGCCATGGTGCTGATAACATACAACGCGGTCATCGGCGGAGATCTACGAGTTCGACATACCC
ACGgCGGTGGCTACGTCAAGGAGCGGTTTTCGGGCAGGGCCCAAGGAAGTTCTACGCGGAGGATAGCCACCGCGCCGGCGGAGGGCCTCGGGGACGTTTCC
GCTCAACGCGCGAGGGGGTGTAGGAGCTACGACGTTGCCCGGCCTTCGCCGGCCTTTCATTCCGAGCCTGCTCGGGAAACTGCCGGCCTTCTC
CAGAAGATAAAGAGGAAGATGAAGGCAACTCGCTCTCGATTACAGCAGCAACGCATCGAAGATTCTCGCCAACAGCTACTACGGCT
ATGCCAGGGCAAGTGGTACTGCGCCGAGTGCGCTTACGGCATGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAAAAGTTCGGTTTTAAAGTCCT
CTATGCAGACACAGACCCCATCGAAGATGCTGAAACAGTCGAAGATGATCTACCTTACGACGAGGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGCGGCAAGGGAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCAGCGAGGGTTTGGAGGCGGAAGTGTCAGGAATTGTCAGGGAAGGGAAAAAGCTGAGCGA
GTTAAAATCCGGCCCGGAGAACTGTTGATAAGGCTACATCGTTCTGAAGGGGTCCGGAAGGATAGGCGACAGGCTACAAGGCCACCGCGGTAGCCATAGCGAAGCGTTTGGCCGGCCAGAGGT
CGGACTACTACATCGGAGAAACTGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGGACAGGAGAACCTGCGCTACCAGAGAGACGAGGAGGAAGAAGAAG
GTGGGCTGAAGCCGAAGGGGGAAGGGAAGAAGAAG//
```

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC GAC GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCC AAG GAG
CTG CAG ATG CTG GAG GAG AAG CAG AAA AAG   // TAG

Sso7d – JDF-3 fusion protein (Fig. 17-RRR)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC GAC GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCC AAG GAG GGC
CTG CAG ATG CTG GAG GAG AAG CAG AAA AAG   //

159/186

Fig. 17 KRR (cont)

```
ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACGCCGAGTTCGAGCCCTACTTCT
ACGCGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGAGATAACCGCGGGAGGAGGCACGGCAGGGTTCGTTAAGGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCGTTGGAGGTCTGGGGTTCCTCACTTCACGCAAGTACATCCGGCACCCGACAAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAAACTCCGATGGAAGAGCTTAAACTCATGTCCTTCGACGATCGAGACGCTCTACCACGAGGGAAGGAGAAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGGTGATAACCGGTGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGAATGATTAA
GCGCTTCTTGAGGGTCGTTAAGGAGGAAGGACCCGGACGGTGCTGATAACCATACAACGGCGACTTCGCCTACGTGAAAAGCGCTGTTGAGGAAGCTTGGGCTGAGCTTT
ACCCTCGGGAGGACGGGAGCCGAAGATACAGCGCCATGGGGACGTTTGCCGGTTCGAGGTGAAGGGCAGGGGTACACTTCGACCTTTATCCAGTTCATAAGGCCGCACCATAA
ACCTTCCGACCTACACCCTTGAGGGTGTATACGAGGCGGGTTTTCGGCAAGGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCGACCGGGCGGGCCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTTACCTACGAGGTTCTTCCCGATGGAGGCCCCAGGCTCATCGGGCGGCCAGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTACACGGAGGAACTCGCTCCAACAAGCCCGACGAGAGGGAGCTGGGCGGAGAAGGGGGGGCT
ACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAAATATCGTGTATCAGGAGGAACGAACTCGGTCGGAAAACCTGCTCGGGGGAAAGG
GCTCAACCGCGAGGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACGAGTTCTGCAAGTTCCTGATTACAGGGAAGCGGGAAACGCTACTACGGCT
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACGTGGAGAAGAATCTCCTCGATTACAGGGAAGGCCTTCCCGCTTCCGGAAACCTGCTCGGAGGAAAGG
ATGCCAGGGGCTAAGAGTGGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTCATCAGAAGATTCTCGCCAACAGCTACTACGGGCT
CTATGCAGACACAGACGATGGGTCTCCACCATTCCTGGAGCGGACGCTGAAACAGTTCTTAAACTATATCAATCGCCGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTTCAGGGCGTTCATCGACGAGGGAGGCAAGAGTAACCACGCGCGGGGCTTGAGGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCGA
GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCAAGGACTCAAGGCCACCGCGGCCCGAACGTAGCCATAGCGAAGCGTTGGCCGCCAGAGGT
GTTAAAATCCGGCCCGGAAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAAGGATAGGCGACCTCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATG
CGGACTACTACCATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCGCTTCGGCTACACCGCAAGGAAGACAGAGGCGCAGGGTCGGGCCTTGGCGC
GTGGCTGAAGCCGAAGGGGGAAGAAGAAGTGA
```

Fig.18

Figure 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci. 98: 6015-6020)

Fig. 19

Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAGAGGTAGACATCTCCAA

GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG

CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC

TGCTGCAGATGCTGGAGAAG

CAGAAAAAG

The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ

MLEKQKK

The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA

GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC

TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG

GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG

TGTCACTAGTCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCC

TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT

GGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT

CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC

CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC

CTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGG

GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCC

AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG

GTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGC

CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC

GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG

GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA

GACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG

CGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT

GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCG

CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC

Fig.19 (cont)

CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCC
CCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC
CCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATCATTA
A

The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA
ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLL
QVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

The DNA sequence encoding the Sso7d-Taq fusion protein
ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA

Fig. 19 (cont')

GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCACTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTG

5   GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCCACGCCAG
AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT

10   GGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
ACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGGTACCT
CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG

15   CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG

20   GAAAGCCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCT

25   CCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
GGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG

30   CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCGC
GAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCC

Fig. 19 (cont)

TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCCCC
CGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC
CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATCATTAA

The amino acid sequence of Sso7d-Taq fusion protein.
MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR
IHVLHPEGYLITPAWLWEKYGLRPDQWADYRALTGDESDNLPGVKGIGEKTARKLL
EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGFVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGA

Fig.19 (cont)

RMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

The DNA sequence encoding the Pfu-Sso7d fusion protein

5   ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA

10 GATGTTCCCACTATTAGAGAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA

15 GGTTGTATCAAGCGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTCGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA

20 TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG

25 AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

30 TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
CAAGATCCTATAGAAAAAATACTCCTTGACTATAGACAAAAAGCGATAAAACTC
TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG

Fig. 19 (con't)

GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC

TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA

TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT

AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG

GAGTGAAATTGCAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA.

CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC

CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC

ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAAACTAGCT

GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA

GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA

AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA

CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG

ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC

GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAGAGGTAGA

CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC

GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC

GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA .

The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERH

GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA

KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID

LPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS

EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI

AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGN

LVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFR

ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK

MKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIE

LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYE

GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE

AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPG

MVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKED

LRYQKTRQVGLTSWLNIKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS

FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

167/186

Fig 19 (cont)

The DNA sequence encoding the Sac7d-ΔTaq fusion protein

ATGATTACGAATTCGACGGTGAAGGTAAAGTTCAAGTATAAGGGTGAAGAGAAA

GAAGTAGACACTTCAAAGATAAAGAAGGTTTGGAGAGTAGGCAAAATGGTGTCC

5   TTTACCTATGACGACAATGGTAAGACAGGTAGAGGAGCTGTAAGCGAGAAAGAT

GCTCCAAAAGAATTATTAGACATGTTAGCAAGAGCAGAAAGAGAGAAGAAAGG

CGGCGGTGTCACTAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCCCGCCGGA

AGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTT

CTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTAT

10 AAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGC

GTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCC

TCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTA

CGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGC

TCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTA

15 CCGGGAGGTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGG

GGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGA

GATCGCCCGCCTCGAGGCCGGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCA

ACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCAT

CGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGC

20 CCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCAC

CAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACG

GGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGT

AGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGA

TCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAG

25 CCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCG

GGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGG

CGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAA

CTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATC

CCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGG

30 TGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG

GAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGGTGAAG

AGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACC

GCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAA

Fig. 19 (cont)

ATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCA

AAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGT

GTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCT

CTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCA

5   TCATTAA

The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA

PKELLDMLARAEREKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL

10 AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL

DPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERP

LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV

LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI

HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY

15 SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG

VLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR

RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARML

LQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG

RGGGGHHHHHH

20

The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA

GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA

AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG

25 GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG

CGGTAAGCGAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG

AAAAAGGGCGGCGGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC

CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG

CCGATCTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCG

30 AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG

ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC

CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCC

CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCC

Fig. 19 (cont)

GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
5   AACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC
TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG
AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
10 GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG
ATGTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
15 ACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCC
20 AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
25 ATCATCATCATTAA

The amino acid sequence of PL-ΔTaq fusion protein

MITNSKKKKKKKRKKRKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
30 AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV

Fig. 19 (cont)

EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAD

5   LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

PRIMER L71F
5'-CCTGCTCTGCCGCTTCACGC-3'

10

PRIMER L71R
5'-GCACAGCGGCTGGCTGAGGA-3'

PRIMER L18015F
15   5'-TGACGGAGGATAACGCCAGCAG-3'

PRIMER L23474R
5'-GAAAGACGA TGGGTCGCTAATACGC-3'

20   ### PRIMER L18015F
5'-TGACGGAGGATAAC GCCAGCAG-3'

PRIMER L29930R
5'-GGGGTTGGAGGTCAATGGGTTC-3'

25

PRIMER L30350F
5'-CCTGCTCTGCCGCTTCACGC-3'

PRIMER L35121R
30   5'-CACATGGTACAGCAAGCCTGGC-3'

PRIMER L2089F
5'-CCCGTATCTGCTGGGA TACTGGC-3

Fig. 19 (con'v')

PRIMER L7112R

5'-CAGCGGTGCTGACTGAATCATGG-3

PRIMER L30350F

5   5'-CCTGCCTGCCGCTTCACGC-3'

PRIMER L40547R

5'-CCAATACCCGTTTCA TCGCGGC-3'

10   **PRIMER H-Amelo-Y**

5'-CCACCTCATCCTGG GCACC-3'

PRIMER H-Amelo-YR

5'-GCTTGAGGCCAACCATCAGAGC-3'

15

Human beta-globin primer 536F

5'-GGTTGGCCAATCTACTCCCAGG-3'

Human beta-globin primer 536R

20   5'-GCTCACTCAGTGTGGCAAAG-3'

Human beta-globin primer 1408R

5'-GATTAGCAAAAGGGCCTAGCTTGG-3'

25

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

```
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1               5                   10                  15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
                20                  25                  30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
            35                  40                  45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
        50                  55                  60
```

FIG. 20A

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                            85   90   95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
                            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
                            115   120   125

Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
                            130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

FIG. 20B

175/186

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180   185   190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210   215   220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245   250   255

FIG. 20C

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340   345   350

FIG. 20D

176/186

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355   360   365

Pro Asn Lys Pro Ser Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370   375   380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385   390   395   400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420   425   430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435   440   445

FIG. 20E

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450   455   460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465   470   475   480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500   505   510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530   535   540

FIG. 20F

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580   585   590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610   615   620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625   630   635   640

FIG. 20G

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675   680   685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725   730   735

FIG. 20H

180/186

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740   745   750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
755   760   765

Trp Leu Asn Ile Lys Lys Ser
770   775

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc   60

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat   120

Fig. 20I

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag   180

gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga   240

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt   300

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc   360

aaagatttgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt   420

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta   480

tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt   540

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct   600

aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta   660

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa   720

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag   780

```
cgagagagag  atgataaaga  gatttctcag  gattatcagg  gagaaggatc  ctgacattat   840

agttacttat  aatggagact  cattcgactt  cccatattta  gcgaaaaggg  cagaaaaact   900

tgggattaaa  ttaaccattg  gaagagatgg  aagcgagccc  aagatgcaga  gaataggcga   960

tatgacggct  gtagaagtca  agggaagaat  acattcgac   ttgtatcatg  taataacaag  1020

gacaataaat  ctcccaacat  acacactaga  ggctgtatat  gaagcaattt  ttggaaagcc  1080

aaaggagaag  gtatacgccg  acgagatagc  aaaagcctgg  gaaagtggag  agaaccttga  1140

gagagttgcc  aaatactcga  tggaagatgc  aaaggcaact  tatgaactcg  ggaaagaatt  1200

ccttccaatg  gaaattcagc  tttcaagatt  agttggacaa  cctttatggg  atgtttcaag  1260

gtcaagcaca  gggaaccttg  tagagtggtt  cttacttagg  aaagcctacg  aaagaaacga  1320

agtagctcca  aacaagccaa  gtgaagagga  gtatcaaaga  aggctcaggg  agagctacac  1380

aggtggattc  gttaaagagc  cagaaaaggg  gttgtgggaa  aacatagtat  acctagattt  1440

tagagcccta  tatccctcga  ttataattac  ccacaatgtt  tctcccgata  ctctaaatct  1500
```

183/186

FIG. 20K

tgaggggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat 1560

ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac 1620

aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc 1680

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta 1740

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg 1800

gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta 1860

tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa 1920

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag 1980

gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac 2040

tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag 2100

agtttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga 2160

FIG. 20L

184/186

agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca 2220

gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa 2280

actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag 2340

aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca 2400

caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt 2460

ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct 2520

aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt 2580

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta 2640

tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc 2700

ttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt 2760

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct 2820

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct 2880

FIG. 20M

185/186

```
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt   2940

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct   3000

acaatttttt cctgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct     3060

ttccgggagt tttgtattgc tctagccaag gttgggggatt tttgaatcct ttaactctgg   3120

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt    3180

taactttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta   3240

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc    3300

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta   3360

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa   3420

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga   3480

aagattgaga tgttcttgg                                               3499
```

186/186

FIG. 20N